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MPSrch_dp protein - protein database search, using Smith-Waterman algorithm
Run on: Mon Mar 8 14:18:50 1999; Maspar time 32.13 Seconds
Tabular output not generated.
Title: >US-08-866-354-38
Description: (1-400) from US08866354.pep
Perfect Score: 3033
Sequence: 1 MVRPLNRPPLPPVLMILL.....PWVPSLFCSTLPLILLSLW 400
Scoring table: PAM 150
Gap 11
Searched: 180763 seqs, 55169189 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: sptrembl8
1:sp-archaea 2:sp-bacteria 3:sp-fungi 4:sp-human
5:sp-invertebrate 6:sp-mammal 7:sp-mhc 8:sp-organelle
9:sp-phage 10:sp-plant 11:sp-rodent 12:sp-unclassified
13:sp-vertebrate 14:sp-virus
Statistics: Mean 46.106; Variance 78.006; scale 0.591
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	3026	99.8	400	4	GDNF FAMILY RECEPTOR A	0.00e+00
2	2358	77.7	400	4	GLIAL CELL LINE-DERIVE	0.00e+00
3	2356	77.7	397	11	GLIAL CELL LINE-DERIVE	0.00e+00
4	2353	77.6	397	11	GLIAL CELL LINE-DERIVE	0.00e+00
5	717	23.6	460	4	RET LIGAND 1.	1.73e-137
6	711	23.4	463	11	GDNF RECEPTOR BETA.	4.81e-136
7	708	23.3	463	11	GDNF-ALPHA/TRNRI-DELT	2.54e-135
8	704	23.2	464	11	GLIAL CELL LINE-DERIVE	2.33e-134
9	701	23.1	464	4	GLIAL CELL LINE-DERIVE	1.23e-133
10	701	23.1	464	4	RET LIGAND 2.	1.23e-133
11	686	22.6	465	4	GPI-LINKED ANCHOR PROT	4.93e-130
12	681	22.5	431	13	GFR RECEPTOR ALPHA 4 P	7.82e-129
13	681	22.5	468	11	GDNF RECEPTOR ALPHA.	7.82e-129
14	113	3.7	130	11	HYPOCRETIN (PREPRO-ORE	2.50e-03
15	113	3.7	130	11	PREPRO-OREXIN.	2.50e-03
16	112	3.7	793	11	PUTATIVE NEURONAL CELL	3.60e-03
17	110	3.6	1321	4	KIA00634 PROTEIN (FRAG	7.39e-03
18	105	3.5	131	6	PREPRO-OREXIN PRECURSOR	4.32e-02
19	102	3.4	941	4	GABA-B RECEPTOR.	1.21e-01
20	101	3.3	183	14	MC142R.	1.70e-01

21	101	3.3	476	4	015481	ACTIVIN TYPE I RECEPTO	1.70e-01
22	101	3.3	487	4	015482	ACTIVIN TYPE I RECEPTO	1.70e-01
23	99	3.3	558	9	017966	C14B1.9.	3.33e-01
24	100	3.3	870	6	002560	SCO-SPONDIN (FRAGMENT)	2.38e-01
25	100	3.3	1969	5	015763	HIBRID HISTIDINE KINAS	2.38e-01
26	96	3.2	131	4	043612	PREPRO-OREXIN.	8.95e-01
27	98	3.2	151	5	024900	EMAREPL2 (FRAGMENT).	4.64e-01
28	97	3.2	151	10	006763	ADRI1 PROTEIN (FRAGMEN	6.45e-01
29	96	3.2	638	6	062707	ENV PROTEIN.	8.95e-01
30	96	3.2	638	6	062705	ENV PROTEIN.	8.95e-01
31	98	3.2	2448	2	051338	PROVEDINE SYNTHETASE	4.64e-01
32	93	3.1	241	11	062076	PHOSPHOLIPASE C BETA 3	2.35e+00
33	94	3.1	505	11	061271	ACTIVIN A RECEPTOR TYP	1.71e-00
34	95	3.1	692	5	077468	HEXAMERIN A (FRAGMENT)	1.24e-00
35	95	3.1	692	5	076211	HEXAMERIN A (FRAGMENT)	1.24e-00
36	95	3.1	692	5	076210	HEXAMERIN A (FRAGMENT)	1.24e-00
37	95	3.1	692	5	077461	HEXAMERIN A (FRAGMENT)	1.24e-00
38	95	3.1	692	5	076209	HEXAMERIN A (FRAGMENT)	1.24e-00
39	94	3.1	1835	5	019346	FILCL.5.	1.71e-00
40	93	3.1	3291	14	066225	OREA AND OREF, COMPLET	5.55e-00
41	92	3.0	355	8	079583	NADH DEHYDROGENASE SUR	5.55e-00
42	92	3.0	355	8	037442	NADH DEHYDROGENASE SUR	5.55e-00
43	92	3.0	355	8	037429	NADH DEHYDROGENASE SUR	5.55e-00
44	92	3.0	355	8	079582	NADH DEHYDROGENASE SUR	5.55e-00
45	92	3.0	914	13	012960	ADAM 13.	5.55e-00

ALIGNMENTS

RESULT ID	1	PRELIMINARY;	PRT;	400 AA.
AC	060609;			
AC	060609;			
DT	01-AUG-1998 (TREMELREL. 07, CREATED)			
DT	01-AUG-1998 (TREMELREL. 07, LAST SEQUENCE UPDATE)			
DT	01-AUG-1998 (TREMELREL. 07, LAST ANNOTATION UPDATE)			
DE	GDNF FAMILY RECEPTOR ALPHA 3.			
GN	GERA3.			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;			
OC	CATARRHINI; HOMINIDAE; HOMO.			
OC	(1)			
RP	SEQUENCE FROM N.A.			
RA	BALOH R.H., GORODINSKY A., GOLDEN J.P., TANSEY M.G., KECK C.L.,			
RA	POPESCU N.C., JOHNSON E.M. JR., MILLBRANDT J.J.			
RL	PROC. NATL. ACAD. SCI. U.S.A. 0:0-0(1998).			
DR	EMBL: AF051767; G2961632; -.			
SO	SEQUENCE 400 AA; 44538 MW; 6DFB5381 CRC32;			

Query Match	99.8%	Score 3026;	DB 4;	Length 400;
Best Local Similarity	99.5%	Pred. No. 0.00e+00;		
Matches 398;	Conservative 1;	Mismatches 1;	Indels 0;	Gaps 0;
Db	1	MVRPLNRPPLPPVLMILLPLPPSPPLAAGDPLPTESRLMNSCLQARRKCOADPTCSAA	60	
Qy	1	MVRPLNRPPLPPVLMILLPLPPSPPLAAGDPLPTESRLMNSCLQARRKCOADPTCSAA	60	
Db	61	YHLDSTSSISTPLSEEPSVPADCLLEAAOQLRNSLLGCKHRRKNOVACLDITYTV	120	
Qy	61	YHLDSTSSISTPLSEEPSVPADCLLEAAOQLRNSLLGCKHRRKNOVACLDITYTV	120	
Db	121	HRAISGNYELDVSPEDYTSKPMKNSLKLMLPPDSGLCKFAMLTGLNDKCDRLK	180	
Qy	121	HRAISGNYELDVSPEDYTSKPMKNSLKLMLPPDSGLCKFAMLTGLNDKCDRLK	180	
Db	121	HRAISGNYELDVSPEDYTSKPMKNSLKLMLPPDSGLCKFAMLTGLNDKCDRLK	180	
Qy	121	HRAISGNYELDVSPEDYTSKPMKNSLKLMLPPDSGLCKFAMLTGLNDKCDRLK	180	
Db	181	AYGACSGPHCQHVCLRLQLTFEKAAPHAAGLLCPAPNDRCCGERRRTIAPNCA	240	
Qy	181	AYGACSGPHCQHVCLRLQLTFEKAAPHAAGLLCPAPNDRCCGERRRTIAPNCA	240	
Db	241	LPVAPNCELRALCSDPLCRSLVDFTCHPNOILGTCAEGRCLRAVIGLGTAM	300	
Qy	241	LPVAPNCELRALCSDPLCRSLVDFTCHPNOILGTCAEGRCLRAVIGLGTAM	300	
Db	301	TRFVSVNTSVSLCTCRGSGNLQEGCEKLEGFHNPCLTEAIAAKRHFSLQSDQM	360	


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      301 TPFTFAVMAHONENPAVPAWPSLFCSTLPLILLISLM 360
      361 PHPTFAVMAHONENPAVPAWPSLFCSTLPLILLISLM 400
      361 PHPTFAVMAHONENPAVPAWPSLFCSTLPLILLISLM 400

RESULT 2
ID 055243: PRELIMINARY: PRT: 397 AA.
AC 055243:
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR FAMILY RECEPTOR ALPHA-3.
GN GFRA3.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC SCIUROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RA WIDENFALK J., TOMAC A., LINDQVIST E., HOFFER B., OLSON L.;
RL SUBMITTED (MAR-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RA NAVILHAN P., BAUDET C., MIKAELS O., SHEN L., WESTPHAL H., ENNFORS P.;
RL PROC. NATL. ACAD. SCI. U.S.A. 0:0-0(1997).
DR EMBL: AF041842; G2921579; -
DR EMBL: AF036163; G2674177; -
SQ SEQUENCE 397 AA; 44302 MW; F77607CF CRC32;

Query Match 77.7%; Score 2358; DB 11; Length 397;
Best Local Similarity 76.8%; Pred. No. 0.00e+00;
Matches 308; Conservative 56; Mismatches 32; Indels 5; Gaps 4;

DB 1 MGLEPRP--PLMLILLVLSLM-LPLGANSLATENFVNSCTQARKKCEANPACAKA 57
  1 MWRPLPRPLPVVLMILLPLPSPLPLAAGDPLPESRLMNSCLQARRKQADPTCSAA 60
  58 YHLSGCTSLSRPLPLESAMSADCLEAAEOLRNSLIDCRCHRRMKHQATCLDIYTWV 117
  61 YHLSGCTSLSRPLPLESAMSADCLEAAEOLRNSLIDCRCHRRMKHQATCLDIYTWV 120
  118 HPARSIGDYELDVSPYEDVTSKPMKMLSKLMLKPPDSDLCKFAMLTLDKCDRLK 177
  121 HRARSIGDYELDVSPYEDVTSKPMKMLSKLMLKPPDSDLCKFAMLTLDKCDRLK 180
  178 AYGEACSGIRCOHRLCLAOIRSFEEKAASHAGLLCPCPPEDACGGERRRNTIAPSCA 237
  181 AYGEACSGIRCOHRLCLAOIRSFEEKAASHAGLLCPCPPEDACGGERRRNTIAPSCA 240
  238 LPSVTNCLDLSRFCRADPLCRSLMDFOTHCHPMIDILTCATEOSRCLRAYLGLIGTAM 297
  241 LPPVANCLELRLCLSDPLCRSLMDFOTHCHPMIDILTCATEOSRCLRAYLGLIGTAM 300
  298 TPFTFAVMAHONENPAVPAWPSLFCSTLPLILLISLM 357
  301 TPFTFAVMAHONENPAVPAWPSLFCSTLPLILLISLM 360
  358 ADSTESVVOONSAPALRLQPLILISFS-ILPLILQTLW 397
  361 PHPTFAVMAHONENPAVPAWPSLFCSTLPLILLISLM 400

RESULT 3
ID 035118: PRELIMINARY: PRT: 397 AA.
AC 035118:
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR FAMILY RECEPTOR ALPHA 3
  (GFRA3).
GN GFRA3 OR GFRA3A-3.

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      301 TPFTFAVMAHONENPAVPAWPSLFCSTLPLILLISLM 360
      361 PHPTFAVMAHONENPAVPAWPSLFCSTLPLILLISLM 400
      361 PHPTFAVMAHONENPAVPAWPSLFCSTLPLILLISLM 400

RESULT 4
ID 035325: PRELIMINARY: PRT: 397 AA.
AC 035325:
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR FAMILY RECEPTOR ALPHA-3.
GN GFRA-3.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC SCIUROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RA TRUPP M., RAYNOSCHER C., IBANEZ C.F.;
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF020305; G2429367; -
DR EMBL: AF020305; G2429367; -
SQ SEQUENCE 397 AA; 44333 MW; F0C0C841 CRC32;

Query Match 77.6%; Score 2353; DB 11; Length 397;

      301 TPFTFAVMAHONENPAVPAWPSLFCSTLPLILLISLM 360
      361 PHPTFAVMAHONENPAVPAWPSLFCSTLPLILLISLM 400
      361 PHPTFAVMAHONENPAVPAWPSLFCSTLPLILLISLM 400

RESULT 4
ID 035325: PRELIMINARY: PRT: 397 AA.
AC 035325:
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR FAMILY RECEPTOR ALPHA-3.
GN GFRA-3.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC SCIUROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RA TRUPP M., RAYNOSCHER C., IBANEZ C.F.;
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF020305; G2429367; -
DR EMBL: AF020305; G2429367; -
SQ SEQUENCE 397 AA; 44333 MW; F0C0C841 CRC32;

Query Match 77.6%; Score 2353; DB 11; Length 397;

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QY 248 CLELRRLCFSDPLCRSLRYDFTCHCHPMDI-LGTGATEQ-SRCLRAYLIGLTAMPNFA 305
DB 298 DSSSLVAPWDCDSNGNLEDDCLKFLNFKMDTCKLNAIOA 339
QY 306 SNVNTSVALLSTCTGRSGNLOECCMELEGFSSHNPCLTEALIA 347

RESULT 7
ID 035748 PRELIMINARY: PRT: 463 AA.
AC 035748: 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DE 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE GDNFR-ALPHA/TRNR1-DELTA PROTEIN.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC SCIROGNAITHI; MORIDAE; MORINAE; RATTUS.
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-HANNOVER;
RA ZHONG J., ANNTES M., HEUMANN R.;
RL SUBMITTED (OCT-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: A002072; E1154274; -
SQ SEQUENCE 463 AA; 51032 MW; 93277F91 CRC32;

Query Match 23.3%; Score 708; DB 11; Length 463;
Best Local Similarity 34.8%; Pred. No. 2,54e-135;
Matches 120; Conservative 74; Mismatches 134; Indels 17; Gaps 14;

DB 1 MFATLTYFALPLDLMLSAEVSQDRL-D-CYRASDOCLEKESCTRYTLROCVAKET 58
QY 14 VMLLMLLPSPPLAAGDPLTESRLMNSCLQARRKCOADPTCSAAVHHLDSCSTISST 73
DB 59 NSLTGLLEAKDCRAMEALKOKSLYNGCRKGRKAKENCLRTYMSQSD-GNDLLE 117
QY 74 PLP-SEEPSVPADCLLAQOLRNSSLIGCMCHRMNOVACDIYTVHARSIGYELD 132
DB 118 DSYE-PVNSRLSDIFRAVPEISVEHISKGNCLDAKACNLDPTCKKRSAYITPCTTS 176
QY 133 VSEYETVTSKPKM--NLSKLMKL-PSDCLAKAMCTLNDCKDLRAKAGECS-G 188
DB 177 MSNEVCNRRKCHALROFDKVPKASHYGLFCSC--RDIACERRRQITVPVSYERE 234
QY 189 -PH--CORHVCRLQLTTFEKAEPHAGLLCPCAPNDRGCGERRRNTIAPCALPVA 245
DB 235 RPNCLSLQSCNTNYICRSLADFTNCPESRSVSNCKLKNYADLLAYSLGIVMP 294
QY 246 -PNCLELRRLCFSDPLCRSLRYDFTCHCHPMDI-LGTGATEQ-SRCLRAYLIGLTAMP 302
DB 295 NYVDSSSLVAPWDCDSNGNLEDDCLKFLNFKMDTCKLNAIOA 339
QY 303 SNVNTSVALLSTCTGRSGNLOECCMELEGFSSHNPCLTEALIA 347

RESULT 8
ID 035977 PRELIMINARY: PRT: 464 AA.
AC 035977: 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DE 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR-BETA.
GN GDNFR-BETA OR RETL2.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
OC SCIROGNAITHI; MORIDAE; MORINAE; RATTUS.
RN (1)
RP SEQUENCE FROM N.A.
RC TRUMP M., RAYNOSCHEK C., IBANEZ C.F.;
RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN/KIDNEY;
RX MEDLINE: 97323356.

RA SANICOLA M., HESSION C.A., WORLEY D.S., CAMILLO P., EHRENFELS C.,
RA WALIS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,
RA PEPINSKY R.B., CATE R.L.;
RT "Glial cell line-derived neurotrophic factor-dependent RET activation
can be mediated by two different cell-surface accessory proteins."
RL PROC. NATL. ACADE. SCI. U.S.A. 94:6238-6243(1997).
RN (3)
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN/KIDNEY;
RA SANICOLA M., HESSION C.A., WORLEY D.S., CAMILLO P., EHRENFELS C.,
RA WALIS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,
RA PEPINSKY R.B., CATE R.L.;
RL SUBMITTED (APR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF005226; G2232252; -
SQ SEQUENCE 464 AA; 51668 MW; B1A2BD11 CRC32;

Query Match 23.2%; Score 704; DB 11; Length 464;
Best Local Similarity 35.3%; Pred. No. 2,33e-134;
Matches 121; Conservative 87; Mismatches 108; Indels 27; Gaps 14;

DB 21 ASPSSLOGE-LHG-WRPQVDCVANELECAESNCSRYTLROCLAG-RDR-NIHLAA
QY 23 PSLPLAAGDPLTESRLMNSCLQARRKCOADPTCSAAVHHLDSCSTISSTPLSEEPSV 73
DB 76 -KEQAALEVLQESPLYDCRCRKGKKELOCLOIYWSHGLTGE-EFEYASPEPVTS 132
QY 83 PADCLLAQOLRNSSLIGCMCHRMNOVACDIYTVHARSIGYELD-DSPHYIV 132
DB 134 RLSDIFRLASIFSGTGTTPAVSTKSNHCLDAKACNLDNCKKRLSSYSISCNREISPM 134
QY 142 -SKWKM-NL-S-K-LM-MLKPSDCLKFLAMCTLNDCKDLRAKAGECS--G 134
DB 194 RGNRRKCHALROFDKVPSEYTYMLFCSC--QDQACERRRQITPLSCYENKERT 194
QY 190 HQRVVCRLQLTTFEKAEPHAGLLCPCAPNDRGCGERRRNTIAPCALPVA-PNC 245
DB 252 LDRLSLCTRDHLCRSLADFTNCPESRSVSNCKLKNYADLLAYSLGIVMP 294
QY 249 LELRLCFSDPLCRSLRYDFTCHCHPM-DIIGTCTEDSR-CLRAYLIGLTAMPNFA 306
DB 312 SNPTGIVSPMCGSGNMECEKFLRDETPNCLNAIOA 354
QY 307 NVNTSVALLS-CTGRSGNLOECCMELEGFSSHNPCLTEALIA 347

RESULT 9
ID 015316 PRELIMINARY: PRT: 464 AA.
AC 015316: 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DE 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR BETA.
GN GDNFR-BETA.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
OC CATARRHINI; HOMINIDAE; HOMO.
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE-FETAL BRAIN;
RA MARTIOVAARA K., SUVANTO P., HORELLI-KUITUNEN N., LINDAHL M.,
RA MOSHNAKOV M., AIRAKSINEN M.S., PALOTIE A., SARIOLA H., SAARMA M.;
RL SUBMITTED (MAR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: U93703; G2228737; -
SQ SEQUENCE 464 AA; 51530 MW; DE80D543 CRC32;

Query Match 23.1%; Score 701; DB 4; Length 464;
Best Local Similarity 35.7%; Pred. No. 1,23e-133;
Matches 115; Conservative 87; Mismatches 95; Indels 25; Gaps 18;

DB 40 CVRANLECAAESNCSRYTLROCLAG-RDR-NIHLAN-KEQAALEVLQESPLYDCRC 95
QY 44 CLQARRKCOADPTCSAAVHHLDSCSTISSTPLSEEPSVPADCLLAQOLRNSSLIGCMC 103

 (TM)

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Mpsrch.un n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Fri Mar 12 01:28:15 1999; Maspar time 3452.68 Seconds
 1362.737 Million cell updates/sec

Tabular output not generated.

Title: >US-08-866-354-37
 Description: (1-1991) from US08866354.seq
 Perfect Score: 1991
 N.A. Sequence: 1 CAACTCAAGGTTATCAT.....CATGATTAACCTTGACTG 1991
 Comp: GTTACGTTTCCAAATTAGTA.....GTACTAATTGGCAACGAC

Scoring table: TABLE default
 Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 602357 seqs, 1181590623 bases x 2

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database:

emb156
 1:em_ba 2:em_fun 3:em_htg 4:em_hum1 5:em_hum2 6:em_in
 7:em_om 8:em_ov 9:em_ov 10:em_pat 11:em_ph 12:em_pi
 13:em_ro 14:em_un 15:em_v1
 genbank110
 16:gb_ba1 17:gb_ba2 18:gb_htg 19:gb_in 20:gb_om 21:gb_ov
 22:gb_pat 23:gb_ph 24:gb_pi1 25:gb_pi2 26:gb_pi1
 27:gb_pi2 28:gb_pi3 29:gb_ro 30:gb_st 31:gb_sts 32:gb_sy
 33:gb_un 34:gb_v1

Statistics: Mean 11.588; Variance 5.819; scale 1.991

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description	Pred. No.
1	1199	60.2	1203	27	AF051767 Homo sapiens GDNF fam1	0.00e+00
2	809	40.6	1867	29	AB008833 Mus musculus GDNF fam1	0.00e+00
3	809	40.5	1884	29	AF051766 Mus musculus GDNF fam1	0.00e+00
4	807	40.5	1911	29	AF036163 Mus musculus glial cel	0.00e+00
5	807	40.5	1932	29	AF020305 Mus musculus GDNF fam1	0.00e+00
6	771	38.7	1194	29	AF020305 Mus musculus glial cel	0.00e+00
7	771	38.7	1244	29	AF041842 Mus musculus glial cel	0.00e+00
8	466	23.4	521	27	HUM2D48G06 Homo sapiens full leng	0.00e+00
9	158	7.9	521	27	HUM2D48G06 Homo sapiens full leng	2.82e-97
10	72	3.6	7218	22	I66494 Sequence 14 from paten	2.16e-30
11	52	2.6	1867	29	AB008833 Mus musculus mRNA for	3.50e-16
12	52	2.6	1884	29	AF051766 Mus musculus GDNF fam1	3.50e-16
13	52	2.6	1932	29	MMTRNR3 Mus musculus mRNA for	3.50e-16

RESULT	LOCUS	DEFINITION	ACCESSION	NID	KEYWORDS	SOURCE	ORGANISM	TITLE	JOURNAL	MEDLINE	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	source
1	AF051767	1203 bp mRNA	AF051767	92961631	g2961631	human.	Homo sapiens	Sequence 14 from paten	8.15e-13							
14	47	2.4	7218	22	I66494		Mus musculus glial cel	Sequence 22 from paten	3.74e-13							
15	46	2.3	1911	29	AF036163		Sequence 5 from paten	2.77e-13								
16	42	2.1	965	22	AR024229		Human glial cell line	1.17e-13								
17	40	2.0	215	22	I28278		Homo sapiens GDNF fam1	1.17e-13								
18	39	2.0	1395	27	HSU93703		Sequence 5 from paten	2.00e-13								
19	39	2.0	1526	28	AF002700		Homo sapiens RET ligand	2.00e-13								
20	39	2.0	2906	28	HSU97145		Sequence 22 from paten	2.00e-13								
21	37	1.9	965	22	I28278		Gallus gallus neuriti	2.00e-13								
22	37	1.9	2933	21	GC090542		Homo sapiens chromosom	2.00e-13								
23	38	1.9	74371	27	AC005369		Rattus norvegicus glia	2.00e-13								
24	36	1.8	1395	29	AF005226		Mus musculus GDNF fam1	2.00e-13								
25	36	1.8	2787	29	AF079143		Mus musculus GDNF fam1	2.00e-13								
26	35	1.8	3206	29	AF030131		Homo sapiens GDNF fam1	2.00e-13								
27	35	1.8	4591	27	AB014534		Homo sapiens GDNF fam1	2.00e-13								
28	35	1.8	74371	27	AC005369		Homo sapiens chromosom	2.00e-13								
29	35	1.8	1321	29	AF079108		Mus musculus GDNF fam1	2.00e-13								
30	33	1.7	1321	29	AF079108		Mus musculus GDNF fam1	2.00e-13								
31	33	1.7	1392	29	AF002701		Mus musculus GDNF fam1	2.00e-13								
32	33	1.7	1405	29	AF079107		Mus musculus GDNF fam1	2.00e-13								
33	34	1.7	2453	29	MMTRP1GN		M. musculus mRNA for ly	2.00e-13								
34	34	1.7	2453	29	MMTRP1GN		Sequence 6 from paten	2.00e-13								
35	33	1.7	3311	22	A48521		Sequence 1 from paten	2.00e-13								
36	33	1.7	3829	27	HUMDPEE		Homo sapiens cyclic AM	2.00e-13								
37	34	1.7	10772	19	AF012089		Drosophila melanogaste	2.00e-13								
38	34	1.7	121804	18	HS229A8		Human DNA sequence ***	2.00e-13								
39	34	1.7	197016	18	HS591N18		Human DNA sequence ***	2.00e-13								
40	34	1.7	197016	18	HS591N18		Human DNA sequence ***	2.00e-13								
41	32	1.6	3200	29	MMU07345		Mus musculus protein l	2.00e-13								
42	32	1.6	3628	27	HSCANPX		Homo sapiens mRNA for	2.00e-13								
43	32	1.6	4263	27	D84103		Human fetus brain mRNA	2.00e-13								
44	32	1.6	4465	27	M1HSDNAPL		H. sapiens mRNA for DN	2.00e-13								
45	32	1.6	5136	29	RMU73458		Rattus norvegicus prot	2.00e-13								

ALIGNMENTS

RESULT	LOCUS	DEFINITION	ACCESSION	NID	KEYWORDS	SOURCE	ORGANISM	TITLE	JOURNAL	MEDLINE	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	source
1	AF051767	1203 bp mRNA	AF051767	92961631	g2961631	human.	Homo sapiens	Sequence 14 from paten	8.15e-13							
14	47	2.4	7218	22	I66494		Mus musculus glial cel	Sequence 22 from paten	3.74e-13							
15	46	2.3	1911	29	AF036163		Sequence 5 from paten	2.77e-13								
16	42	2.1	965	22	AR024229		Human glial cell line	1.17e-13								
17	40	2.0	215	22	I28278		Homo sapiens GDNF fam1	1.17e-13								
18	39	2.0	1395	27	HSU93703		Sequence 5 from paten	2.00e-13								
19	39	2.0	1526	28	AF002700		Homo sapiens RET ligand	2.00e-13								
20	39	2.0	2906	28	HSU97145		Sequence 22 from paten	2.00e-13								
21	37	1.9	965	22	I28278		Gallus gallus neuriti	2.00e-13								
22	37	1.9	2933	21	GC090542		Homo sapiens chromosom	2.00e-13								
23	38	1.9	74371	27	AC005369		Rattus norvegicus glia	2.00e-13								
24	36	1.8	1395	29	AF005226		Mus musculus GDNF fam1	2.00e-13								
25	36	1.8	2787	29	AF079143		Mus musculus GDNF fam1	2.00e-13								
26	35	1.8	3206	29	AF030131		Homo sapiens GDNF fam1	2.00e-13								
27	35	1.8	4591	27	AB014534		Homo sapiens GDNF fam1	2.00e-13								
28	35	1.8	74371	27	AC005369		Homo sapiens chromosom	2.00e-13								
29	35	1.8	1321	29	AF079108		Mus musculus GDNF fam1	2.00e-13								
30	33	1.7	1321	29	AF079108		Mus musculus GDNF fam1	2.00e-13								
31	33	1.7	1392	29	AF002701		Mus musculus GDNF fam1	2.00e-13								
32	33	1.7	1405	29	AF079107		Mus musculus GDNF fam1	2.00e-13								
33	34	1.7	2453	29	MMTRP1GN		M. musculus mRNA for ly	2.00e-13								
34	34	1.7	2453	29	MMTRP1GN		Sequence 6 from paten	2.00e-13								
35	33	1.7	3311	22	A48521		Sequence 1 from paten	2.00e-13								
36	33	1.7	3829	27	HUMDPEE		Homo sapiens cyclic AM	2.00e-13								
37	34	1.7	10772	19	AF012089		Drosophila melanogaste	2.00e-13								
38	34	1.7	121804	18	HS229A8		Human DNA sequence ***	2.00e-13								
39	34	1.7	197016	18	HS591N18		Human DNA sequence ***	2.00e-13								
40	34	1.7	197016	18	HS591N18		Human DNA sequence ***	2.00e-13								
41	32	1.6	3200	29	MMU07345		Mus musculus protein l	2.00e-13								
42	32	1.6	3628	27	HSCANPX		Homo sapiens mRNA for	2.00e-13								
43	32	1.6	4263	27	D84103		Human fetus brain mRNA	2.00e-13								
44	32	1.6	4465	27	M1HSDNAPL		H. sapiens mRNA for DN	2.00e-13								
45	32	1.6	5136	29	RMU73458		Rattus norvegicus prot	2.00e-13								

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BASE COUNT 236 a 419 c 309 g 239 t

ORIGIN

	Query Match	Similarity	90.28%	Score	1199	DB	27	Length	1203	
	Best Local	Similarity	90.28%	Pred	No.	00+00				
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O	203	ATGGTGGCCCGCCCTGTAACCCGCGACCCGCTGCGCGCCGCTGATCTGATATTGCTCTGCTG	262							
D	61	CTGCGCGCGCTGCGCGCTCTCTCTGACACCGGAGAACCCCTTCCACAGAAAGCCGACTC	120							
O	263	CTGCGCGCGCTGCGCGCTCTCTCTGACACCGGAGAACCCCTTCCACAGAAAGCCGACTC	322							
D	121	ATGAACAGCTCTCTTCACAGCGCAGAGAGAAAGTGCAGAGCTGATATCCACTCGACTGCTGCC	180							
O	323	ATGAACAGCTCTCTTCACAGCGCAGAGAGAAAGTGCAGAGCTGATATCCACTCGACTGCTGCC	382							
D	181	TACCAACACCTGAGATCTCTGCACTCTAGCATTAAGACCCCACTGACCTCTAGAGAGCT	240							
O	383	TACCAACACCTGAGATCTCTGCACTCTAGCATTAAGACCCCACTGACCTCTAGAGAGCT	442							
D	241	TGGGTCCTGCTGATGCTGCTGAGGACACACAGCAACTCAGAAAGCTCTCTGTAAGGC	300							
O	443	TGGTTCCTGCTGATGCTGCTGAGGACACACAGCAACTCAGAAAGCTCTCTGTAAGGC	502							
D	301	TGCATGTGCCACACCGCGCATGCTGTAACCCAGGTTGGCTGCTTGGACATCTATTGGACGTT	360							
O	503	TGCATGTGCCACACCGCGCATGCTGTAACCCAGGTTGGCTGCTTGGACATCTATTGGACGTT	562							
D	361	CACGTCGCCCGCAGCCTTGTAACATATAGTACTGATGCTCTCCCTATGAAGACACAGT	420							
O	563	CACGTCGCCCGCAGCCTTGTAACATATAGTACTGATGCTCTCCCTATGAAGACACAGT	622							
D	421	ACCAACAAACCTTGGAAATGATCTCAGCAACAGCAATGCTCAACACGACTCAGAC	480							
O	623	ACCAACAAACCTTGGAAATGATCTCAGCAACAGCAATGCTCAACACGACTCAGAC	682							
D	481	CTTGCCTCAAGTTGGCATGCTGTGTACTCTCAATGACAAAGTGTAGCCGCTCGCAG	540							
O	683	CTTGCCTCAAGTTGGCATGCTGTGTACTCTCAATGACAAAGTGTAGCCGCTCGCAG	742							
D	541	GCCTAACGGGGAGGGCTGCTCGCGGCCCACTGACAGCGCCACAGTCTGCTACGACAGTG	600							
O	743	GCCTAACGGGGAGGGCTGCTCGCGGCCCACTGACAGCGCCACAGTCTGCTACGACAGTG	802							
D	601	CTCACTTCTTCTGAGAAAGCCGCGAGCCCAACGCGGACGCGGCTGCTACTGTGCCATGT	660							
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D	661	GCCCCCAACGACCGGGGCTGCGGGGAGCGCGCGGCGCAACACCATGCCCCCACTGCGCG	720							
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D	721	CTGCGCGCTGAGGCCCCCACTGCTGAGAGTGGGCGGCGCTGCTTCTGCAACCGGTT	780							
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O	983	TGCAGATCAGCGCTGCTGATTTCCAGAACCCACTGCTCATTCATGAGACATCTTAGAAGT	1042							
D	841	TGTGCACAGAGACAGTCCAGATGTTACGAGCATTAAGTGGGCTGATTTGGACATGCAATG	900							

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QY	1103	ACCCCAACTTTGTATGAAATGTCAACACCAAGTGTGCTTAACTGACACTGCCGAGGC	1162
Db	961	AGTGCACACTGACGAGGAGTGTGAATGTGTGAAGGGTCTTCTCCACACACCCCTGC	1020
QY	1103	AGTGCACACTGACGAGGAGTGTGAATGTGTGAAGGGTCTTCTCCACACACCCCTGC	1020
Db	1021	CTCAGGAGGCGCATTTGACGTAGATGCGTTTTCACAGCCAACTCTTCTCCAGAGATTT	1000
QY	1223	CTCAGGAGGCGCATTTGACGTAGATGCGTTTTCACAGCCAACTCTTCTCCAGAGATTT	1000
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QY	1283	CCACACCTTACCTTTGCTGTGATGGCACACCAAGATGAAAACCTGCTGTGAGCCGAA	1000
Db	1141	CCCTGGGGGCGCTCTCTTCTCTCGACAGCGTCCCTGATTCGCTCTGAGCTATTC	1000
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Db	215	CCGCTTGCAGAGGTGCTCTCCACAGCACTGTGGGCTCTCTCAGCTCCAGTTTAAGCAGGCC	274
Qy	355	CCCACTGTAGAGTGTGCTGCTACCAACACCTGTGAATCTCTGACTCTAGATTAAGCAACCCA	424
Db	275	CTGCCCCYTAGAGAGTCTGCCATGTCTGCAGACTGCTCTTAGAGGCAACGAACAATCTAGG	334
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Db	335	AACAGCTCTGTGAAGACTCAGAGTCCGATTCGAGCGATGAAAGCAACAAAGTACCTGTCTG	394
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Db	395	GACATTTATTGGACCGTTTCACCCCTGCCCGAAGCCTTGTGACTACGAGTTGGATGTCTCA	454
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Db	455	CCCTATGAAGACAGTGAACAGACAGCAAAACCTGGAAAAATGAATCTTAGCAATTTGACATG	514
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Db	515	CTCAAAACAGAGCTGGAGACTGTGCTCTCAATTTTGTATGCTGTACTCTTACAGCAAG	574
Qy	665	CTCAAAACAGAGCTGAGACCTGTGCTCTCAATTTTGTATGCTGTACTCTTACATGACAG	724
Db	575	TGTGACCGCCCTGCGCAAGGCTTACGGGGAGGACATCTCAAGGGAATCCGCTGCCACGCCAC	634
Qy	725	TGTGACCGCGCTGCGCAAGGCTTACGGGGAGGCTGTCTCGGGGCCCACTGTCCACGCGCAC	784
Db	635	CTCTGACTAGCCACAGTGGCGCTCCCTTTTGAAGAAAGCAGACAGATCTCCAGCTCAGGGT	694
Qy	785	GCTCTGCTCAGGCAAGTCTCTACTTTCTTGAAABAAGCCGCGGAGCCCAAGCGGAGGGG	844
Db	695	CTGCTGTGTGTCTCTGCTCCACACGAAGAATGCGGGCTGTGGGAGAGCGGCGCTTAACAC	754
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Db	815	TGCGGTGGGAGCCCTTTGTGCAGATCAAGGCTGATGAGTCTCCAGACCACCTGTATCTCT	874
Qy	965	TGCTTCTCGAACCGCTTTTGCAGATCAAGGCTGATGAGTCTCCAGACCACCTGTATCTCT	1024
Db	875	ATGAGACATCTTGGGACTGTGTGCAACTGACAGACATTCAGATGTCTGGGGCAATACCTGGG	934
Qy	1025	ATGAGACATCTTGGGACTGTGTGCAACTGACAGACATTCAGATGTCTGAGACATACCTGGG	1084
Db	935	CTGATTTGGAGCTGCGCATTAACCCCAAACTTCATCGCAAGGCTCAACACTACTGTGCTTA	994
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Db	995	AGCTGACACTGCCGAGGAGCGAGGCAACCTTACAGAGACGATGTGAACAGCTGGAAAGGCC	1054
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Db	1055	TTCCTCCACAACCCCTGCGCTGTGTGAAGGCACTTGCACATTAAGATGCTTCCACAGACAG	1114
Qy	1205	TTCCTCCACAACCCCTGCGCTCAAGAGGCACTTGCACATTAAGATGCTTCCACAGCCA	1264
Db	1115	CTCTTCTCCAGAGCTGGGCAACTTACTTTTCACTGGTGTGACAGACGAAGAACAGCAAC	1174
Qy	1265	CTCTTCTCCAGAGCTGGGCAACCCCTCAACTTTCTGTGATGGCAACAGATGAATAAC	1324
Db	1175	CCGTGCTGAGAGCTGAGGCGGAGGCTACCAATTTCTTCTTCCATCTCTCCCTTGAT	1234
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Db	1235	CTGTGCAGACACCCTGCTGTAAGCTGGGCTTCCTCAGGGTCTTTTGCTCTCCACACACC	1294
Oy	1385	CTGCTCGAGACCATTGATGACTTGACTTCCCAGGGGCCCTCT-TCCTCTCCACACACC	1443
Db	1295	CAGACTGATTTGGACGCTGTGCTGGGAGAACAACCGCACGCTGTGAAGAAGACGAGC	1354
Oy	1444	CAGGTGACCTTGACAGCCACAGAGGGGTGAGAAAGAACAGCAGCAGAGAGGTGCAGT	1503
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Oy	1504	GCGC 1507	
RESULT	5		
LOCUS	MTRNR3	1932 bp	mRNA
DEFINITION	Mus musculus mRNA for TGF-beta-related neurotrophic factor receptor-3.		
ACCESSION	y15110		
NID	g2959855		
KEYWORDS	neurotrophic receptor; TGF-beta related protein; trnk-3 gene		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eulipotyphla; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
TITLE	Zhong, J., Aniles, M., Tolle, A. and Heumann, R.		
JOURNAL	Molecular cloning of a new member of Trk family		
REFERENCE	Unpublished		
AUTHORS	2 (bases 1 to 1932)		
TITLE	Zhong, J.		
JOURNAL	Direct Submission		
REFERENCE	Submitted (11-OCT-1997) J. Zhong, Molecular Neurobiology, NCI/NIH, Ruhr-University Bochum, Universitaetstr. 150, D-4620 Bochum, FRG		
COMMENT	Related publication: Lennon G. et al, Genomics 33, 151-155, 1998		
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ORIGIN			441 t
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Best local Similarity	82.1%; Pred. No. 0.0e+00;		
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Db	175	GCACAGAGAGAGGTTTGGAAACAGCTGTACCCAGAGCAGAGAAAGAAATGCGAGGCTAAT	234
Oy	305	CCACAGAGAAAGCCGACTCATGACACACTGTCTCCAGGCGCAGAGAGAAAGTCCAGGCTGAT	364

[illegible][illegible]

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D	564	TGTGACGCCCTGGCCAAAGGGCTACGGGAGGAGCATGCTACAGGGAATCCGCTGCCAGGCCAC	623
Oy	725	TGTGACGGCGTGGCCAAAGGGCTACGGGAGGAGCGTGC GGGGCCCCAAGTGGACGGCCAC	784
D	634	CTCTGCTTAGCCCAAGCTGCGCTCTTTTGTAGAAGGACAGAGATCCCAGCTCAAGGT	683
Oy	785	GCTGCGCTCAGGACAGCTCTCATCTTTCTTGTGAAGAAGGCCGCCAGGCCACAGCGAGGGC	844
D	684	CTGCGCGCTGTGCTCCCTGACCACGAAGATGCGGGGCTGTGGGAGAGGGGGGTAAACAC	743
Oy	845	CTGCTACTGTGTCATGATGCTATGCCCCAACAGACCGGGGCTGCGGGAGAGCGCGCCACACAC	904
D	744	ATCGCCCCCACTTGGCGCTGCGCTCTTGTAAACCCCAATTGCTGTGATGCGGAGACTTC	803
Oy	905	ATCGCCCCCACTTGGCGCTGCGCGCTGTGGCCCCCAACTGCTGTGAGCTGCGGGCGCTC	964
D	804	TGCGGTGGGACCTTTGTGCAATATCACGGCTATGGAATCTCCAGACCCACATGTCATCT	863
Oy	965	TGCTTCTCCGACCGGCTTTGCAATCACGGCTGTGATTTCCAGACCCACAGTCCATCC	1024
D	864	ATGGAATCCTTTGGGACTTGTGCAACAGACAGATCCAGATGTGCGGGCATACCTGGGG	923
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D	924	CTGATTTGGGACTGTCATGACCCCAACTTCATCAGCAAGGTCAACACTATGTTGCCTTA	983
Oy	1085	CTGATTTGGGACTGTCATGACCCCAACTTCGCAAGATTCACACAGTGTTCCTTA	1144
D	984	AGCTGACCTTGGGAGGCGAGCGCAACTTACAGAGAGATGTGAACAGCTGGAAAAGTTC	1043
Oy	1145	AGCTGACCTTGGGAGGCGAGCGCAACTTACAGAGAGATGTGAAGTGTGAAGGGTTTC	1204
D	1044	TTTCTCCAGAACCCCTGCTCTGTGTGAGGCGCATTTGACAGCTAAGATGCGTTTCCACAGACAG	1103
Oy	1205	TTTCTCCAGAACCCCTGCTCTGTGTGAGGCGCATTTGACAGCTAAGATGCGTTTCCACAGACCA	1264
D	1104	CTTCTTCTCCAGAGACTGGGCGAGACTTACTTTTTCACTGTGTGACGACAGACAAGCAAC	1163
Oy	1265	CTTCTTCTCCAGAGACTGGGCGAGACTTACTTTTTCACTGTGTGATGTGACACACCAATGAAAAA	1324
D	1164	CCTGCTGTGAGACATGCAAGGCCAGGCTTACCATCTTTCTTCCATACCTTCCCTTGATT	1223
Oy	1325	CCTGCTGTGAGGCCAGACGCCCTGGGTGCTCTTCTTCTTCCGACAGCTTCCCTTGATT	1384
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RESULT	8		
LOCUS	HUMDZ48G06	521 bp	mRNA PRI 29-AUG-1998
DEFINITION	Homo sapiens full length insert cDNA clone ZD48G06.		
ACCESSION	AF086292		
NID	G3483637		
KEYWORDS	FLI_CDNA.		
SOURCE	human.		
ORGANISM	Homo sapiens		
Eukaryote:	Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;		
Primates; Catarrhini; Hominiidae; Homo.			
REFERENCE	1 (bases 1 to 521)		
AUTHORS	Moesner,J., Tan,F., Marra,M., Kucaba,T., Vendell,M., Martin,J., Matsui,G., Bowles,L., Wylie,T., Bowers,Y., Stepien,M., Theising,B., Getzel,S., Allen,M., Underwood,K., Chappell,J., Person,B., Gibbons,M., Harvey,N., Page,D., Chamberlain,A., Morales,R., Schurk,R., Ritzer,E., Kohn,S., Swaller,T., Behmer,K., Hiller,L., Wilson,R. and Waterston.R.		
TITLE	Full Clone Sequencing of the Longest Available Member from Each UniGene Cluster		

JOURNAL REFERENCE	Unpublished 2 (bases 1 to 521)
AUTHORS	Waterston, R.
TITLE	Direct Submission
JOURNAL	Submitted (24-APR-1998) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63110
COMMENT	SUBMITTED BY: Genome Sequencing Center Department of Genetics Washington University St. Louis MO 63108, USA http://genome.wustl.edu/gsc mailto:est@watson.wustl.edu
NOTE: This sequence represents the full insert of this cDNA. attempt has been made to verify whether this corresponds to a full-length of the original mRNA from which it was derived. We have tried to obtain double-stranded, or double chemistry, across the entire clone, but potentially, there are areas in the sequence where this level of coverage was not achieved. Nevertheless, we are confident of the accuracy of this sequence in all regions of low quality, as defined by PHRAP (P. Green, in preparation), were visually inspected and edited accordingly. Consensus quality values for this sequence have been submitted separately.	
The location of this clone is unknown.	
FEATURES	Location/Qualifiers
source	1..521 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_id="Scares.fetal_heart_NBH19w" /clone_image="IMAGE:343930" 143 t
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ORIGIN	
Query Match	23.4% Score 466; DB 27; Length 521;
Best Local Similarity	99.6% Pred. No. 0.00e+00;
Matches	466; Conservative 0; Mismatches 2; Indels 0; Gaps 0
41	GGAGAGCTAAGGGTTATGACCTCCAGATCCTTACTGCTGACGTCCTCATTCCTCCACC 100
1521	GGAGAGCTAAGGGTTATGACCTCCAGATCCTTACTGCTGACGTCCTCATTCCTCCACC 1580
101	CCATCTCCATCTTGATTCACTGCTGCCCTCTTGCTGGTGGCCACAAATTAGCATGTCATC 160
1581	CCATCTCCATCTTGATTCACTGCTGCCCTCTTGCTGGTGGCCACAAATTAGCATGTCATC 1640
161	TGGTGTACCAAGCTCCACAAAGCCCTTTGTGAGCCCTTCTTACTACTACAGATCA 220
1641	TGGTGTACCAAGCTCCACAAAGCCCTTTGTGAGCCCTTCTTACTACTACAGATCA 1700
221	CCAGATCTAATTAAGTTAGCCTTTCTCTAATGCAATCCAGATTAGGGTTAGGTAGGAG 280
1701	CCAGATCTAATTAAGTTAGCCTTTCTCTAATGCAATCCAGATTAGGGTTAGGTAGGAG 1760
281	GACTGGGCTTCTGAGGAGCCTTGAAGAATCATCTCTTTGTGAAGAAGCCTCTGCC 340
1761	GACTGGGCTTCTGAGGAGCCTTGAAGAATCATCTCTTTGTGAAGAAGCCTCTGCC 1820
341	CCTGCTCTCTCTCTGAGTGGAGATGAAACAACTGCTGCACTGCCCTGTCCCGG 400
1821	CCTGCTCTCTCTCTGAGTGGAGATGAAACAACTGCTGCACTGCCCTGTCCCGG 1880
401	ATCTGCGCGAATCTGGGCACTAGAGACTGGACCTGTGGGCTTCTTATTCATAT 460
1881	ATCTGCGCGAATCTGGGCACTAGAGACTGGACCTGTGGGCTTCTTATTCATAT 460
461	ATTGCTCTAAGATCTCTGAGGCTTGTGATCATGATTAACCTTTACT 510
1941	ATTGCTCTAAGATCTCTGAGGCTTGTGATCATGATTAACCTTTACT 1940

LOCUS	9	HMMZD48G06	521 bp	mRNA	PR1	29-AUG-1998
DEFINITION		Homo sapiens full length insert cDNA clone ZD48G06.				
ACCESSION		AF086292				
NID		93483637				
KEYWORDS		FLI cDNA.				
SOURCE		human.				
ORGANISM		Homo sapiens				
REFERENCE		Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
AUTHORS		1 (bases 1 to 521) Moessner,J., Tan,F., Marra,M., Kucaba,T., Yandell,M., Martin,J., Math,G., Bowles,L., Wylie,T., Bowers,Y., Steptoe,M., Thelings,B., Geisel,S., Allen,M., Underwood,K., Chappell,J., Person,B., Gibbons,M., Harvey,N., Pape,D., Chamberlain,A., Morales,R., Schurt,R., Ritter,E., Kohn,S., Swaller,T., Behmyer,K., Hilder,L., Wilson,R. and Waterston,R.				
TITLE		Full Clone Sequencing of the Longest Available Member from Each Unigene Cluster				
JOURNAL		Unpublished				
REFERENCE		2 (bases 1 to 521) Waterston,R.				
AUTHORS		Direct Submission				
TITLE		Submitted (24-AUG-1998) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA				
JOURNAL		http://genome.wustl.edu/gsc mailto:est@watson.wustl.edu				
COMMENT		SUBMITTED BY: Genome Sequencing Center Department of Genetics Washington University St. Louis MO 63108, USA http://genome.wustl.edu/gsc mailto:est@watson.wustl.edu				
FEATURES		<p>NOTICE: This sequence represents the full insert of this cDNA. attempt has been made to verify whether this corresponds to the full-length of the original mRNA from which it was derived. We have tried to obtain double-stranded, or double chemistry sequence across the entire clone, but potentially, there are areas in the sequence where this level of coverage was not achieved. Nevertheless, we are confident of the accuracy of this sequence as all regions of low quality, as defined by PHRAP (P. Green, in preparation), were visually inspected and edited accordingly. The consensus quality values for this sequence have been submitted separately.</p> <p>The location of this clone is unknown.</p> <p>location/Qualifiers</p> <p>1..521</p> <p>/organism="Homo sapiens"</p> <p>/db_xref="taxon:9606"</p> <p>/clone_1lb="Scores_fetal_heart_NbH19W"</p> <p>/clone="IMAGE:343930"</p>				
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Best Local Similarity		97.1%;	Pred. No. 2,82e-97;			
Matches	168;	Conservative	0;	Mismatches	4;	Indels 1; Gaps 1;
339	CCCCCTGCTCTCTCTCTGATGGAGGATGAAACAACTGCTGCACTGCCCTTCCC	398				
CP	173 CCCCCTCG-CTCTCCCTCGATGGAGGATGAAACAACTGCTGCTGCACTGCCCTTCCC	115				
DB	399 GGATCTCGCGAACAATCTGGGATCAGAGAGCGAGCGTGGGCTTGTATTCTGA	458				
CP	114 GGATCTCGCGAACAATCTGGGATCAGAGAGCGAGCGTGGGCTTGTATTCTGA	55				
DB	459 TTATGTCTTAAGTCTCTGCGCTTGTGATCAATTAACCTTTGACTT	511				
CP	54 TTATGTCTTAAGTCTCTGCGCTTGTGATCAATTAACCTTTGACTT	2				
RESULT	10					

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LOCUS      166494      7218 bp      DNA
DEFINITION Sequence 14 from patent US 5670367.
ACCESSION  166494
NID        92724471
KEYWORDS
SOURCE
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 7218)
AUTHORS    Dörner, F., Schefflinger, F. and Falkner, F. Gunter.
TITLE      Recombinant fowipox virus
JOURNAL    Patent: US 5670367-A 14 23-SEP-1997;
FEATURES
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ORIGIN
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Best Local Similarity 0.9%; Pred. No. 2,16e-30;
Matches 3; Conservative 209; Mismatches 140; Indels 0; Gaps
Dn 1087 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1541 CCTCAGATCCTTACTGTCAGTCAGTCATTCCTCCACCCCATCTCCATCTATTA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dn 1147 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1601 TGTGCCCCCTCTGTGTGGCCACATTTAGCATGTATCTGTGTGTCAGCTGAC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dn 1207 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1661 AAGCCCTTGTGAGCCCTTCTCTGACTACAGAGATCACCAGATTAATAAATA
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Dn 1267 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1721 CTCTCTCATTCATTCACATTCAGATTAAGGTTAGGTAAGGAGAGATGGTTC
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Dn 1327 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1781 CCTGAAGATCATTCCTCTTGTGTGAAGAGGCTCTGCCCCCTGCTCTCTCT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dn 1387 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYGTAC
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 1841 GGAGGATGGAAGAACTACTGCTGCACTCCCTGTCGCCGATCCTGCCGAAC
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RESULT 11
LOCUS      AB008833      1867 bp      mRNA
DEFINITION Mus musculus mRNA for GFRalpha-3, complete cds.
ACCESSION  AB008833
NID        92627159
KEYWORDS   GFRalpha-3.
SOURCE     Mus musculus (strain:C57BL/6) adult heart cDNA to mRNA.
ORGANISM   Mus musculus
           Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
           Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (sites)
AUTHORS    Nomoto, S., Ito, S., Yang, L.X. and Kitchin, K.
TITLE      Molecular cloning and expression analysis of GFR alpha-3, a novel
JOURNAL    cDNA related to GDNFR alpha and NTN9 alpha
MEDLINE    Blochem. Biophys. Res. Commun. 244 (3), 849-853 (1998)
REFERENCE  2 (bases 1 to 1867)
AUTHORS    Nomoto, S.
TITLE      Direct Submission
JOURNAL    Submitted (13-NOV-1997) to the DDBJ/EMBL/Genbank databases.
AUTHORS    Nomoto, RIKEN (The Institute of Physical and Chemical Research),
           Bio-Mimetic Control Research Center, 2271-130 Anagahora,
           Shimodamari, Moriyama-ku, Nagoya, Aichi 463, Japan
           (E-mail:nomoto@nagoya.riken.go.jp, Tel:81-52-736-5864,
           Fax:81-52-736-5865)
FEATURES
Location/Qualifiers

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source

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LOTLM"

BASE COUNT 384 a 572 c 474 g 437 t

ORIGIN

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Best Local Similarity 76.5%; Pred. No. 3,50e-16;
Matches 75; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

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Db 1824 CAAAATCCCCTAGTCCCTGGCTGATGATTAACATT 1861
|| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Cp 44 AAAGTCTCTCTGGGCTCTTGATCATGATTAACCTT 7
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RESULT 12
LOCUS AF051766 1884 bp mRNA ROD 26-JUN-1998
DEFINITION Mus musculus GDNF family receptor alpha 3 mRNA, complete cds.
ACCESSION AF051766
NID g261629
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1884)
AUTHORS Baloh,R.H., Gorodlinsky,A., Golden,J.P., Tansey,M.G., Keck,C.L.,
Popescu,N.C., Johnson,E.M. Jr. and Milbrandt,J.
TITLE GfRalpha3 is an orphan member of the GDNF/neurturin/persephin
receptor family
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (10), 5801-5806 (1998)
MEDLINE 98245162
REFERENCE 2 (bases 1 to 1884)
AUTHORS Baloh,R.H. and Milbrandt,J.D.
TITLE Direct Submission
JOURNAL Submitted (03-MAR-1998) Pathology, Washington University, 660 South
Euclid Ave, St. Louis, MO 63110, USA
FEATURES
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Db 1840 CCAAAATGCCCTAGTCCCTTGGGCTCATGATTAACATTT 1878
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Best Local Similarity 91.6%; Pred. No. 0.00e+00;
Matches 1244; Conservative 0; Mismatches 112; Indels 2; Gaps 1;

12 CGGGGGCCAGGCGGAGGAGCGCTGTCGATCCCGGCGGCCA--CCCGCATGGGCT 69
15 CGAGCCCGACAGGCGAGCGCTGCGGGTCGCGGCTCCAGACCCGCGCATGGGCT 74
70 CTCCTGGAGCGGAGCTCCACTGCTGATGATCTCTGCTGCTGCTGCTGCTGCT 129
75 CTCGGGAGCGCGGAGCGCGCGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 134
130 GCCACTGGAGCAGAGAACTCCCTGGCCACAGAGAAAGTTTGTGAACAGCTTACCA 189
135 ACCCTTGGAGCAGAGAACTCCCTGCCACAGAGAAAGCTTGTGAACAGCTTACCA 194
190 GGGCAGAAAGAAATGCGGCGTAACTCCGCTTGAAGGCTCCACAGCAAGCTGGGCTC 249
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1275 GGTCTTTGCTCTCTCCAGCAGACCTGCTGAGACTGATTTGAGCTGGGAGAGACTC 1275
DB 1330 GCCAGCTGTGAGAGAGAGCAGCGCTGCTACACAGCA 1367
1335 GCTGCGCTGTGAGAGAGAGCAGCGCTGCTACACAGCA 1372
RESULT 5
LOCUS AF041842 1244 bp mRNA 16-JUN-1998
DEFINITION Mus musculus glial cell line-derived neurotrophic factor family
ACCESSION AF041842
NID 92921578
KEYWORDS house mouse.
SOURCE Mus musculus.
ORGANISM Mus musculus.
REFERENCE 1 (bases 1 to 1244)
AUTHORS Widenfalk, J., Tomac, A., Lindqvist, E., Hoffer, B. and Olson, L.
TITLE GFRA1pha-3, a protein related to GFRA1pha-1, is expressed in developing peripheral neurons and ensheathing cells
JOURNAL Eur. J. Neurosci. 10 (4), 1508-1517 (1998)
MEDLINE 98420233
REFERENCE 2 (bases 1 to 1244)
AUTHORS Tomac, A., Hoffer, B. and Olson, L.
TITLE Direct Submission
JOURNAL Submitted (07-JAN-1998) Neuroscience, Karolinska Institute, Doktorstingen 12, Stockholm 17171, Sweden
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Db 209 VPSEYTYRLFLSCCK-DQA-CAEPRROTIVPFCSEYDEKEKPNCLDRNYCRADHLRSRL 266
Oy 204 AASHHAGILLCPACVEDAGCGRRNTIAPSCALSYA-PNDDLRSRCRADPLCRSLR 262
Db 267 ADHANCAQSFQSLTSCPGDNVACAGSYGLIGFDMTPYVDASTTSTISPMSCSKS 326
Oy 263 MDQTHCHP-MDLGTCATEOSR-CLRAYGLIGTAMTPNFIKNTVTALG--CTCRGS 318
Db 327 GNLEECEKFLRDETFENPCPLNIOA 352
Oy 319 GNLDCECEOLEKFSQNPCLMEIAIA 344

RESULT 2
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AC 008842:
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE NEUTURIN RECEPTOR ALPHA PRECURSOR (NTRN-ALPHA) (TGF-
DE BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 2) (GNF RECEPTOR BETA)
DE (GNFR-BETA).
DE GFR2 OR GDNFR OR TRNR2.
GN MUS MUSCULUS (MOUSE).
OS EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA;
OC EUTHERIA: RODENTIA.
OC (1)
RN SEQUENCE FROM N.A.
RX MEDLINE: 97325791.
RA BALOH R.H., TANSEY M.G., GOLDEN J.P., CREEDON D.J.,
RA HEUCKROTH R.O., KECK C.L., ZIMONJIC D.B., POPESCU N.C.,
RA JOHNSON E.M. JR., MILBRANDT J.;
RL NEURON 18;793-802(1997).
CC -1- FUNCTION: RECEPTOR FOR NEUTURIN, MEDIATES THE NTRN-INDUCED
CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR. ALSO ABLE
CC TO MEDATE GNF SIGNALING THROUGH THE RET TYROSINE KINASE
CC RECEPTOR.
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
CC SIMILARITY).
CC -1- TISSUE SPECIFICITY: NEURONS OF THE SUPERIOR CERVICAL AND DORSAL
CC ROOT GANGLIA, AND ADULT BRAIN AND TESTIS. LOW LEVEL IN THE SPLEEN
CC AND IN THE ADRENAL.
CC -1- ALTERNATIVE PRODUCTS: A SHORT FORM IS PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.
CC DR EMBL: AF002701; G2145082;
CC DR MGD: MGI:1195462; GFR2;
CC KW RECEPTOR; GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL;
CC KW ALTERNATIVE SPLICING.
CC FT SIGNAL 1 21
CC FT CHAIN 22 443
CC FT PROPEP 444 463
CC FT CARBOHYD 52 52
CC FT CARBOHYD 357 357
CC FT CARBOHYD 413 413
CC FT LIPID 443 443
CC FT VARSPLC 14 146
CC FT SEQUENCE 463 AA; 51598 MW; 0A2165C0 CRC32;

Query Match 25.7%; Score 762; DB 1; Length 463;
Best Local Similarity 37.9%; Pred. No. 1,006-163;
Matches 122; Conservative 75; Mismatches 100; Indels 25; Gaps 18

Db 40 CVRAHELCAASNCSSRYTLROC---LAGR-DRTMTLANNECQAALVELDSEPLYDRC 95
Oy 41 CTQARKKEANPACAAVYOHLDSCPSLSSPLPSEGSATSNACLEAAQOLNNSLIDRC 100

```

[illegible]

 W E I R D
 (TM)

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Mparch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Mar 8 14:07:03 1999; Maspar time 36.88 Seconds

Tabular output not generated. 694.165 Million cell updates/sec

Title: >US-08-866-354-36
 Description: (1-464) from US08866354.pep
 Perfect Score: 3386
 Sequence: 1 MILANVFCLFFLDLTLRL.....RAPSALTVLSVLMKAL 464

Scoring table:
 PAM 150
 Gap 11

Searched: 180763 seqs, 55169189 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: sptrembl8
 1:sp-archaea 2:sp-bacteria 3:sp-fungi 4:sp-human
 5:sp-invertebrate 6:sp-mammal 7:sp-mhc 8:sp-organelle
 9:sp-phage 10:sp-plant 11:sp-rodent 12:sp-unclassified
 13:sp-vertebrate 14:sp-virus

Statistics: Mean 46.920; Variance 70.591; scale 0.665

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	3383	99.9	464	015328	RET LIGAND 2.	0.00e+00
2	3365	99.4	464	015316	GLIAL CELL LINE-DERIVE	0.00e+00
3	3332	95.5	464	015316	GLIAL CELL LINE-DERIVE	0.00e+00
4	1535	45.3	464	035748	GNFR-ALPHA/TRNRI-DELT	0.00e+00
5	1527	45.1	464	035748	GNFR RECEPTOR ALPHA	0.00e+00
6	1520	44.9	464	035748	GNFR RECEPTOR ALPHA	0.00e+00
7	1508	44.5	464	035748	GNFR RECEPTOR ALPHA	0.00e+00
8	1499	44.3	464	035748	GNFR RECEPTOR ALPHA	0.00e+00
9	1392	41.1	431	093512	GNFR RECEPTOR ALPHA 4 P	0.00e+00
10	782	23.1	397	035118	GLIAL CELL LINE-DERIVE	6.73e-172
11	782	23.1	397	035118	GLIAL CELL LINE-DERIVE	6.73e-172
12	782	23.1	397	035118	GLIAL CELL LINE-DERIVE	6.73e-172
13	705	20.8	400	060609	GNFR FAMILY RECEPTOR A	5.00e-151
14	107	3.2	1713	088349	LATEIN TGF BETA BINDIN	6.41e-03
15	110	3.2	2090	094247	CODED FOR BY C. ELEGAN	1.98e-03
16	110	3.2	2153	094246	CODED FOR BY C. ELEGAN	1.98e-03
17	105	3.1	192	001471	COSMID C04E6.	1.39e-02
18	103	3.0	287	076101	CD97_HUMAN, PARTIAL CD	2.98e-02
19	101	3.0	483	082704	1-CYCLOPROPANE-1-CARBO	6.32e-02
20	98	2.9	165	069417	HYPOTHETICAL 17.8 KD P	1.91e-01

RESULT ID	1	PRELIMINARY:	PRT:	464 AA.
AC	015328;			
DT	01-JAN-1998 (TREMREL. 05, CREATED)			
DT	01-JAN-1998 (TREMREL. 05, LAST SEQUENCE UPDATE)			
DT	01-NOV-1998 (TREMREL. 08, LAST ANNOTATION UPDATE)			
DE	RET LIGAND 2.			
GN	RET2.			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA: PRIMATES:			
OC	CATARRHINI: HOMINIDAE: HOMO.			
RN	[1]			
RC	SEQUENCE FROM N.A.			
RC	TISSUE=LIVER:			
RA	MEDLINE: 97322356.			
RA	SANTICOLA M., HESSON C. A., MORLEY D. S., CARMILO P., EHRENFELS C.,			
RA	WALUS L., ROBINSON S., JAKORSKI G., WEI H., TIZARD R., WHITTY A.,			
RA	PEPINSKI R. B., CAPE R. L.;			
RT	"Glial cell line-derived neurotrophic factor-dependent RET activation			
RT	can be mediated by two different cell-surface accessory proteins."			
RL	PROC. NATL. ACAD. SCI. U.S.A. 94:6238-6243(1997).			
DR	EMBL: U97145: G2282028: -			
SO	SEQUENCE 464 AA: 51543 MW: 288A8BD8 CRC32:			

ALIGNMENTS

Query Match 1
 Best Local Similarity 99.9%; Score 3383; DB 4; Length 464;
 Matches 462; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Query Match	1	Score	3383	DB 4	Length	464
1	MILANVFCLFFLDLTLRLSPSSLOGLPGLGMPVDCVAVNELCAESNCSSNRRL	99.9%	3383	DB 4	Length 464	
2	MILANVFCLFFLDLTLRLSPSSLOGLPGLGMPVDCVAVNELCAESNCSSNRRL	99.9%	3383	DB 4	Length 464	
3	MILANVFCLFFLDLTLRLSPSSLOGLPGLGMPVDCVAVNELCAESNCSSNRRL	99.9%	3383	DB 4	Length 464	
4	MILANVFCLFFLDLTLRLSPSSLOGLPGLGMPVDCVAVNELCAESNCSSNRRL	99.9%	3383	DB 4	Length 464	
5	MILANVFCLFFLDLTLRLSPSSLOGLPGLGMPVDCVAVNELCAESNCSSNRRL	99.9%	3383	DB 4	Length 464	
6	MILANVFCLFFLDLTLRLSPSSLOGLPGLGMPVDCVAVNELCAESNCSSNRRL	99.9%	3383	DB 4	Length 464	
7	MILANVFCLFFLDLTLRLSPSSLOGLPGLGMPVDCVAVNELCAESNCSSNRRL	99.9%	3383	DB 4	Length 464	
8	MILANVFCLFFLDLTLRLSPSSLOGLPGLGMPVDCVAVNELCAESNCSSNRRL	99.9%	3383	DB 4	Length 464	
9	MILANVFCLFFLDLTLRLSPSSLOGLPGLGMPVDCVAVNELCAESNCSSNRRL	99.9%	3383	DB 4	Length 464	
10	MILANVFCLFFLDLTLRLSPSSLOGLPGLGMPVDCVAVNELCAESNCSSNRRL	99.9%	3383	DB 4	Length 464	
11	MILANVFCLFFLDLTLRLSPSSLOGLPGLGMPVDCVAVNELCAESNCSSNRRL	99.9%	3383	DB 4	Length 464	
12	MILANVFCLFFLDLTLRLSPSSLOGLPGLGMPVDCVAVNELCAESNCSSNRRL	99.9%	3383	DB 4	Length 464	
13	MILANVFCLFFLDLTLRLSPSSLOGLPGLGMPVDCVAVNELCAESNCSSNRRL	99.9%	3383	DB 4	Length 464	
14	MILANVFCLFFLDLTLRLSPSSLOGLPGLGMPVDCVAVNELCAESNCSSNRRL	99.9%	3383	DB 4	Length 464	
15	MILANVFCLFFLDLTLRLSPSSLOGLPGLGMPVDCVAVNELCAESNCSSNRRL	99.9%	3383	DB 4	Length 464	
16	MILANVFCLFFLDLTLRLSPSSLOGLPGLGMPVDCVAVNELCAESNCSSNRRL	99.9%	3383	DB 4	Length 464	
17	MILANVFCLFFLDLTLRLSPSSLOGLPGLGMPVDCVAVNELCAESNCSSNRRL	99.9%	3383	DB 4	Length 464	
18	MILANVFCLFFLDLTLRLSPSSLOGLPGLGMPVDCVAVNELCAESNCSSNRRL	99.9%	3383	DB 4	Length 464	
19	MILANVFCLFFLDLTLRLSPSSLOGLPGLGMPVDCVAVNELCAESNCSSNRRL	99.9%	3383	DB 4	Length 464	
20	MILANVFCLFFLDLTLRLSPSSLOGLPGLGMPVDCVAVNELCAESNCSSNRRL	99.9%	3383	DB 4	Length 464	

Db 241 CSYEDKEKNCJDLRGVCTDHLCSRLADFHANCRASTQVTSQPADNYQACLSYAGM 300
 241 CSYEDKEKNCJDLRGVCTDHLCSRLADFHANCRASTQVTSQPADNYQACLSYAGM 300
 Db 301 IGFDMTPNVYDSSPTGIVVSPMCSCGSGNMEECEKFLRDTENPCLRNAIOAFGNGTD 360
 301 IGFDMTPNVYDSSPTGIVVSPMCSCGSGNMEECEKFLRDTENPCLRNAIOAFGNGTD 360
 Db 361 VVNSPKGSPFOATQAPRVEKTPSLPDDLSSTSGTSTVTTCTSVQOGLKANKSKELSM 420
 361 VVNSPKGSPFOATQAPRVEKTPSLPDDLSSTSGTSTVTTCTSVQOGLKANKSKELSM 420
 Db 421 CFTELTNTIIPGSKNKVIRKNSGSPRRARPSAALTIVSLMLKIAL 464
 421 CFTELTNTIIPGSKNKVIRKNSGSPRRARPSAALTIVSLMLKIAL 464
 Db 421 CFTELTNTIIPGSKNKVIRKNSGSPRRARPSAALTIVSLMLKIAL 464
 421 CFTELTNTIIPGSKNKVIRKNSGSPRRARPSAALTIVSLMLKIAL 464

RESULT 2
 ID 015316 PRELIMINARY: PRT: 464 AA.
 AC 015316:
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
 DE GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR BETA.
 GN GDNF-BETA.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
 CC CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-FETAL BRAIN;
 RA WARTIOVAARA K., SUVANTO P., HORELLI-KUITUNEN N., LINDAHL M.,
 RA MOSHINIAKOV M., AIRASINEN M.S., PALOTIE A., SARIOLA H., SAARMA M.;
 RL SUBMITTED (MAR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: U93703; G2328737; -;
 SQ SEQUENCE 464 AA; 51530 MW; DE60D543 CRC32;

Query Match 99.4%; Score 3365; DB 4; Length 464;
 Best Local Similarity 99.1%; Pred. No. 0.00e+00;
 Matches 460; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 1 MILANAFCLFFLDELTLRLSLASPSLSQGLHGMPPVDCVANELCAESNCSSRYRTL 60
 1 MILANAFCLFFLDELTLRLSLASPSLSQGLHGMPPVDCVANELCAESNCSSRYRTL 60
 Db 61 RCLAGRDNTMLANKKECOALEVLOESPPLYDCRCKRGKMKKELOCIQIYMSIHGLTEGE 120
 61 RCLAGRDNTMLANKKECOALEVLOESPPLYDCRCKRGKMKKELOCIQIYMSIHGLTEGE 120
 Db 61 RCLAGRDNTMLANKKECOALEVLOESPPLYDCRCKRGKMKKELOCIQIYMSIHGLTEGE 120
 61 RCLAGRDNTMLANKKECOALEVLOESPPLYDCRCKRGKMKKELOCIQIYMSIHGLTEGE 120
 Db 121 EYFASPEPYTSRLSDIFRLASIFSGTGADPVVSAKSNHCLDAKACNLNDNCKLRSS 180
 121 EYFASPEPYTSRLSDIFRLASIFSGTGADPVVSAKSNHCLDAKACNLNDNCKLRSS 180
 Db 121 EYFASPEPYTSRLSDIFRLASIFSGTGADPVVSAKSNHCLDAKACNLNDNCKLRSS 180
 121 EYFASPEPYTSRLSDIFRLASIFSGTGADPVVSAKSNHCLDAKACNLNDNCKLRSS 180
 Db 181 YISICNREISTPERCNRKCHKALROFFDRVPSEYTYRLMFCSCODACAERRRDTILPS 240
 181 YISICNREISTPERCNRKCHKALROFFDRVPSEYTYRLMFCSCODACAERRRDTILPS 240
 Db 181 YISICNREISTPERCNRKCHKALROFFDRVPSEYTYRLMFCSCODACAERRRDTILPS 240
 181 YISICNREISTPERCNRKCHKALROFFDRVPSEYTYRLMFCSCODACAERRRDTILPS 240
 Db 241 CSYEDKEKNCJDLRGVCTDHLCSRLADFHANCRASTQVTSQPADNYQACLSYAGM 300
 241 CSYEDKEKNCJDLRGVCTDHLCSRLADFHANCRASTQVTSQPADNYQACLSYAGM 300
 Db 241 CSYEDKEKNCJDLRGVCTDHLCSRLADFHANCRASTQVTSQPADNYQACLSYAGM 300
 241 CSYEDKEKNCJDLRGVCTDHLCSRLADFHANCRASTQVTSQPADNYQACLSYAGM 300
 Db 301 IGFDMTPNVYDSSPTGIVVSPMCSCGSGNMEECEKFLRDTENPCLRNAIOAFGNGTD 360
 301 IGFDMTPNVYDSSPTGIVVSPMCSCGSGNMEECEKFLRDTENPCLRNAIOAFGNGTD 360
 Db 301 IGFDMTPNVYDSSPTGIVVSPMCSCGSGNMEECEKFLRDTENPCLRNAIOAFGNGTD 360
 301 IGFDMTPNVYDSSPTGIVVSPMCSCGSGNMEECEKFLRDTENPCLRNAIOAFGNGTD 360
 Db 361 VVNSPKGSPFOATQAPRVEKTPSLPDDLSSTSGTSTVTTCTSVQOGLKANKSKELSM 420
 361 VVNSPKGSPFOATQAPRVEKTPSLPDDLSSTSGTSTVTTCTSVQOGLKANKSKELSM 420
 Db 361 VVNSPKGSPFOATQAPRVEKTPSLPDDLSSTSGTSTVTTCTSVQOGLKANKSKELSM 420
 361 VVNSPKGSPFOATQAPRVEKTPSLPDDLSSTSGTSTVTTCTSVQOGLKANKSKELSM 420
 Db 421 CFTELTNTIIPGSKNKVIRKNSGSPRRARPSAALTIVSLMLKIAL 464
 421 CFTELTNTIIPGSKNKVIRKNSGSPRRARPSAALTIVSLMLKIAL 464
 Db 421 CFTELTNTIIPGSKNKVIRKNSGSPRRARPSAALTIVSLMLKIAL 464
 421 CFTELTNTIIPGSKNKVIRKNSGSPRRARPSAALTIVSLMLKIAL 464

RESULT 3
 ID 035977 PRELIMINARY: PRT: 464 AA.
 AC 035977:
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR-BETA.
 GN GDNF-BETA OR RETL2.
 OS RATTUS NORVEGICUS (RAT).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
 CC SCUROGNATHI; MORIDAE; MORINAE; RATTUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TRUPP M., RAYNOSCHER C., IBANEZ C.F.;
 RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN/KIDNEY;
 RX MEDLINE: 97322356.
 RA SANICOLA M., HESSION C.A., WORLEY D.S., CARMILLO P., EHRENFELS C.,
 RA WALUS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,
 RA PERINSKY R.B., CATE R.L.;
 RT "Glial cell line-derived neurotrophic factor-dependent RET activation
 can be mediated by two different cell-surface accessory proteins.";
 RT PROC. NATL. ACAD. SCI. U.S.A. 94:6238-6243(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN/KIDNEY;
 RA SANICOLA M., HESSION C.A., WORLEY D.S., CARMILLO P., EHRENFELS C.,
 RA WALUS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,
 RA PERINSKY R.B., CATE R.L.;
 RL SUBMITTED (APR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AF005226; G2323252; -;
 DR EMBL: U97143; G2282024; -;
 SQ SEQUENCE 464 AA; 51668 MW; B1A2BD11 CRC32;

Query Match 95.5%; Score 3232; DB 11; Length 464;
 Best Local Similarity 94.2%; Pred. No. 0.00e+00;
 Matches 437; Conservative 18; Mismatches 9; Indels 0; Gaps 0;

Db 1 MILANAFCLFFLDELTLRLSLASPSLSQGLHGMPPVDCVANELCAESNCSSRYRTL 60
 1 MILANAFCLFFLDELTLRLSLASPSLSQGLHGMPPVDCVANELCAESNCSSRYRTL 60
 Db 61 RCLAGRDNTMLANKKECOALEVLOESPPLYDCRCKRGKMKKELOCIQIYMSIHGLTEGE 120
 61 RCLAGRDNTMLANKKECOALEVLOESPPLYDCRCKRGKMKKELOCIQIYMSIHGLTEGE 120
 Db 61 RCLAGRDNTMLANKKECOALEVLOESPPLYDCRCKRGKMKKELOCIQIYMSIHGLTEGE 120
 61 RCLAGRDNTMLANKKECOALEVLOESPPLYDCRCKRGKMKKELOCIQIYMSIHGLTEGE 120
 Db 121 EYFASPEPYTSRLSDIFRLASIFSGTGADPVVSAKSNHCLDAKACNLNDNCKLRSS 180
 121 EYFASPEPYTSRLSDIFRLASIFSGTGADPVVSAKSNHCLDAKACNLNDNCKLRSS 180
 Db 121 EYFASPEPYTSRLSDIFRLASIFSGTGADPVVSAKSNHCLDAKACNLNDNCKLRSS 180
 121 EYFASPEPYTSRLSDIFRLASIFSGTGADPVVSAKSNHCLDAKACNLNDNCKLRSS 180
 Db 181 YISICNREISTPERCNRKCHKALROFFDRVPSEYTYRLMFCSCODACAERRRDTILPS 240
 181 YISICNREISTPERCNRKCHKALROFFDRVPSEYTYRLMFCSCODACAERRRDTILPS 240
 Db 181 YISICNREISTPERCNRKCHKALROFFDRVPSEYTYRLMFCSCODACAERRRDTILPS 240
 181 YISICNREISTPERCNRKCHKALROFFDRVPSEYTYRLMFCSCODACAERRRDTILPS 240
 Db 241 CSYEDKEKNCJDLRGVCTDHLCSRLADFHANCRASTQVTSQPADNYQACLSYAGM 300
 241 CSYEDKEKNCJDLRGVCTDHLCSRLADFHANCRASTQVTSQPADNYQACLSYAGM 300
 Db 241 CSYEDKEKNCJDLRGVCTDHLCSRLADFHANCRASTQVTSQPADNYQACLSYAGM 300
 241 CSYEDKEKNCJDLRGVCTDHLCSRLADFHANCRASTQVTSQPADNYQACLSYAGM 300
 Db 301 IGFDMTPNVYDSSPTGIVVSPMCSCGSGNMEECEKFLRDTENPCLRNAIOAFGNGTD 360
 301 IGFDMTPNVYDSSPTGIVVSPMCSCGSGNMEECEKFLRDTENPCLRNAIOAFGNGTD 360
 Db 301 IGFDMTPNVYDSSPTGIVVSPMCSCGSGNMEECEKFLRDTENPCLRNAIOAFGNGTD 360
 301 IGFDMTPNVYDSSPTGIVVSPMCSCGSGNMEECEKFLRDTENPCLRNAIOAFGNGTD 360
 Db 361 VVNSPKGSPFOATQAPRVEKTPSLPDDLSSTSGTSTVTTCTSVQOGLKANKSKELSM 420
 361 VVNSPKGSPFOATQAPRVEKTPSLPDDLSSTSGTSTVTTCTSVQOGLKANKSKELSM 420
 Db 361 VVNSPKGSPFOATQAPRVEKTPSLPDDLSSTSGTSTVTTCTSVQOGLKANKSKELSM 420
 361 VVNSPKGSPFOATQAPRVEKTPSLPDDLSSTSGTSTVTTCTSVQOGLKANKSKELSM 420
 Db 421 CFTELTNTIIPGSKNKVIRKNSGSPRRARPSAALTIVSLMLKIAL 464
 421 CFTELTNTIIPGSKNKVIRKNSGSPRRARPSAALTIVSLMLKIAL 464
 Db 421 CFTELTNTIIPGSKNKVIRKNSGSPRRARPSAALTIVSLMLKIAL 464
 421 CFTELTNTIIPGSKNKVIRKNSGSPRRARPSAALTIVSLMLKIAL 464


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RESULT 4
ID 035748 PRELIMINARY: PRT: 463 AA.
AC 035748:
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE GDNFR-ALPHA/TRNRI-DELTA PROTEIN.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCUROGNATHI; MURIDAE; MURINAE; RATTUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HANNOVER;
RA ZHONG J., ANNIES M., HEUMANN R.;
RL SUBMITTED (OCT-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AJ002072; E1154274;
SQ SEQUENCE 463 AA; 51032 MW; 93277F91 CRC32;

Query Match 45.3%; Score 1535; DB 11; Length 463;
Best Local Similarity 48.4%; Pred. No. 0.00e+00;
Matches 224; Conservative 101; Mismatches 115; Indels 23; Gaps 19;

Db 2 FLATIPALPLDILMSAEVSG-GDRLDCKVAKSDQCKECSCTKRTLRQCVAGKETNF 60
QY 12 FLDDTLRLSLAPSSLOQEGELHGMWRPVDCCVRANELCAESNCSRYRTLROCLAGRDN- 70
Db 61 SLTSGLEAKDECRSMEALKKOKSLYNCRCRKGKKEKNCRLRYSMYOSL-QGNDLLED 119
QY 71 TM--LANK-ECQALAEVQESPLYDCRCRKGKKEKELCLOLIYSHLGEGEFEYAS 126
Db 120 PYPENRSLDIFRAVP-F-TSVEHI-S-KGNCLDAKACNLDDCTCKRYSAITPTCT 174
QY 127 PYPETSLSDIFRLASIFSGTGAIPVYSAKSNHCLDAKACNLNDCKLRSSYSTICN 186
Db 175 TSMS-NEVCNRRKCKKALROFPDKVPANHSIGMLFCSCRDIACTERRRQTIIVPCSYER 233
QY 187 REISPTERCNRKCKHAKALROFEDRVSEYTYRMLFCSCDQACABRRRQTIIPSCSYDXK 246
Db 234 ERPNCLSLDSCKTNYICRSRLADFTNCOPEBSRSVSNCKLENYADCLLAYSGLGTYMT 293
QY 247 EKPNCCLDRGVCRTDHLRSLADHANCRASTYOTVSCPADNYOACISYAGMIGFDMT 306
Db 294 PNYVDS-S-LSVAPMCDSCNSGNDLEDCLKFLNFKNTCLKNAIQAFNGSDVTMMOP 351
QY 307 PNYVDSPTGIYVSPMCGCRSGNNEECEKLRDFTENPCLRNIAQAFNGNTNVPSPK 366
Db 352 APPVOTTTATTTAFRVANKPLGPAAGSENEIPTHYLPPCANLQAKLSNVSGSTHCLLS 411
QY 367 GPSFOATQAPRY-E-KTSPSLPDLDSDTS-LGTSVITTCSTVOEGKLANKSKELSMCFT 423
Db 412 DSDEKDLGAGASSHITTKS-MA-APPSGLSSLPVLMITALA 452
QY 424 E-LITNIIIPGSKNKVIKENSGSPRSAPALTVLSVLMK-LA 463

RESULT 5
ID 035246 PRELIMINARY: PRT: 468 AA.
AC 035246:
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE GDNFR RECEPTOR ALPHA.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCUROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57; TISSUE-LIVER;
RA DEY B.K., WONG Y.W., TOO H.P.;
RL NEUROREPORT 9:0-0(0001).
DR [2]

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RP SEQUENCE FROM N.A.
RC STRAIN-C57; TISSUE-LIVER;
RA DEY B.K., WONG Y.W., TOO H.P.;
RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF014117; G2624961;
SQ SEQUENCE 468 AA; 51751 MW; AFDE6A1 CRC32;

Query Match 45.1%; Score 1527; DB 11; Length 468;
Best Local Similarity 48.1%; Pred. No. 0.00e+00;
Matches 216; Conservative 104; Mismatches 111; Indels 18; Gaps 15;

Db 16 LMSAEVSG-GDRLDCKVAKSDQCKECSCTKRTLRQCVAGKETNLSLGLAKDECRS 74
QY 26 LQGPGLHGMWRPVDCCVRANELCAESNCSRYRTLROCLAGRDN-TM--LANK-ECQA 80
Db 75 AMELKOKSLYNCRCRKGKKEKNCRLRYSMYOSL-QGNDLLEDSPYEPVNRSLDIFR 133
QY 81 ALEVQSSPLYDCRCRKGKKEKELCLOLIYSHLGEGEFEYASYPVTRSLDIFR 140
Db 134 AVPRISVFOOVEHISKGNCLDAKACNLDDCTCKRYSAITPTCTSMS-NEVCNRRKC 192
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QY 436 VIKPNSGSPRSAPALTVLSVLMK-LA 463

RESULT 6
ID 043912 PRELIMINARY: PRT: 465 AA.
AC 043912:
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE GPI-LINKED ANCHOR PROTEIN.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
CATARRHINI; HOMINIDAE; HOMO.
RN [1]
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RA ANGRIST M., JING S., BOK S., BENTLEY K., NALLASAMY S., HALUSHKA M.,
RA FOX G.M., CHAKRAVARTI A.;
RL GENOMICS 0:0-0(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-MEDULLARY THYROID CARCINOMA TUMOR;
RA SHEFFELDAINE S.E., KHORANA P.N., SCHULTZ P.N., HUANG E., THOBE N., HU 2.J.,
RA FOX G.M., JING S., CORE G.J., GAGEL R.F.;
RL HUM. GENET. 0:0-0(1998).
DR EMBL: AF038420; G2921545;
DR EMBL: AF038411; G2921545; JOINED.
DR EMBL: AF038412; G2921545; JOINED.
DR EMBL: AF038413; G2921545; JOINED.
DR EMBL: AF038414; G2921545; JOINED.
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RESULT 3
LOCUS HSU93703 1395 bp mRNA PRI 01-JUN-1995
DEFINITION Human glial cell line-derived neurotrophic factor (GDNF-beta) mRNA, complete cds.
ACCESSION U93703
MID 9228736
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1395)
AUTHORS Martlovare K., Suvanto P., Horelli-Kuitunen N., Lindahl M., Moshnyakov M., Alirakinen M.S., Palotie A., Sariola H. and Saksela M.
TITLE Cloning, mRNA distribution and chromosomal localisation of the human glial cell line-derived neurotrophic factor beta, homologue to GDNF-alpha
JOURNAL 2 (bases 1 to 1395)
AUTHORS Suvanto P., Martlovare K. and Saarma M.
TITLE Direct Submision
JOURNAL Submitted (06-MAR-1997) Molecular Neurobiology, Institute of Biotechnology, JP 56, University of Helsinki 00014, Finland
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Query Match 28.8%; Score 1218; DB 29; Length 2787;

Best Local Similarity 88.7%; Pred. No. 0.00e+00;

Matches 1425; Conservative 0; Mismatches 177; Indels 5; Gaps 5;

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RESULT

5

LOCUS AF005226 1395 bp mRNA ROD 02-01-1999
 DEFINITION Rattus norvegicus glial cell line-derived neurotrophic factor
 receptor-beta (GDNF-beta) mRNA, complete cds.

ACCESSION AF005226
 MID 92232251

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 1395)

2 (bases 1 to 1395)

3 (bases 1 to 1395)

4 (bases 1 to 1395)

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AUTHORS	Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
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JOURNAL	Baloh, R.H., Tansey, M.G., Golden, J.P., Creodon, D.J.,		
MEDLINE	Heuchercich, R.O., Keck, C.L., Zimonic, D.B., Popescu, N.C.,		
REFERENCE	Johnson, E.M. Jr. and Milbrandt, J.		
AUTHORS	through Ret		
TITLE	Neuron 18 (5), 793-802 (1997)		
JOURNAL	97325791		
MEDLINE	2 (bases 1 to 1392)		
REFERENCE	Baloh, R.H. and Milbrandt, J.D.		
AUTHORS	Direct Submission		

JOURNAL Submitted (06-MAR-1997) Pathology, Washington University, 660 South
Euclid Ave, Box 8118, St. Louis, MO 63110, USA

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DEFINITION Mus musculus glial cell line derived neurotrophic factor family
receptor alpha 2b (Gfra2) mRNA, complete cds.
ACCESSION AF079107
NID 93941703
KEYWORDS
SOURCE mouse.
ORGANISM Mus musculus.
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Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1405)
Wong, Y.W. and Too, H.P.
Identification of mammalian Gfra-2 splice isoforms
Neuroreport 9 (17) (1998) In press

activation can be mediated by two different cell-surface accessory proteins
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (12), 6238-6243 (1997)
 MEDLINE 9732356
 REFERENCE 2 (bases 1 to 3616)
 AUTHORS Santicola, M., Hession, C.A., Worley, D.S., Camillo, P., Ehrenfels, C., Walsby, L., Robinson, S., Jaworski, G., Wei, H., Tizard, R., Whitley, A., Pepinsky, R.B. and Gale, R.L.

TITLE Direct Submission
 JOURNAL Submitted (11-APR-1997) Molecular Genetics, BIOGEN, 14 Cambridge Center, Cambridge, MA 02142, USA

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gene
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KEYWORDS
 SOURCE house mouse.
 ORGANISM Mus musculus.

REFERENCE
 1 (bases 1 to 2549)
 Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS
 Dey, B.K., Wong, X.W. and Too, H.P.
 Cloning of a novel murine isoform of the glial cell line factor
 neurotrophic factor receptor
 Neuroreport 9 (1) (1998) In press

REFERENCE
 2 (bases 1 to 2549)
 Dey, B.K., Wong, X.W. and Too, H.P.
 Direct Submission
 Submitted (15-JUL-1997) Biochemistry, 10 Kent Ridge Crest Drive,
 Singapore 119260, Singapore

TITLE JOURNAL
 AUTHORS
 Dey, B.K., Wong, X.W. and Too, H.P.
 Direct Submission
 Submitted (15-JUL-1997) Biochemistry, 10 Kent Ridge Crest Drive,
 Singapore 119260, Singapore

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gene
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 Primates; Catarrhini; Hominoidea; Homo.
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 AUTHORS Sheffield, S.E., Khorana, S., Schultz, P.N., Huang, E., Thobe, N.,
 Hu, J., Fox, G.M., Jing, S., Cole, G.J., and Gage, R.F.
 JOURNAL Hum. Genet. (1998) In press
 REFERENCE 2 (bases 1 to 1619)
 AUTHORS Sheffield, S.E., Khorana, S., Schultz, P.N., Huang, E., Thobe, N.,
 Hu, J., Fox, G.M., Jing, S., Cole, G.J., and Gage, R.F.
 TITLE Direct Submission

JOURNAL Submitted (08-JAN-1998) Endocrinology-Box 15, M.D. Anderson Cancer
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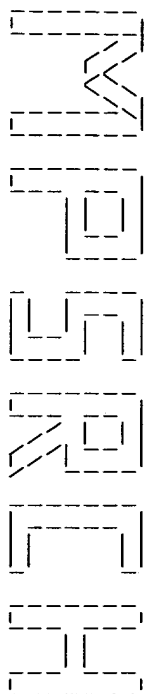
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Job time : 15745 secs.



(TM)

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MSPrch_n n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Fri Mar 12 06:14:28 1999; Maspar time 3837.26 Seconds

Tabular output not generated. 1364.111 Million cell updates/sec

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Scoring table: TABLE default

Gap 6

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Post-processing: Minimum Match 0%

Listing first 45 summaries

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13:em_ro 14:em_un 15:em_v1

genbank110

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Statistics: Mean 12.065; Variance 15.384; scale 0.784

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	1478	66.7	2787	29	Rattus norvegicus RET	0.00e+00
2	1355	61.2	1395	29	Rattus norvegicus gila	0.00e+00
3	1252	56.5	1392	29	Mus musculus GDNF fam1	0.00e+00
4	1159	52.3	2906	28	Mus musculus GDNF fam1	0.00e+00
5	1157	52.2	1526	28	Homo sapiens RET ligand	0.00e+00
6	1116	50.4	1395	27	Human gila1 cell line-	0.00e+00
7	944	42.6	1405	29	Mus musculus gila1 cel	6.39e-297
8	870	39.3	1321	29	Mus musculus gila1 cel	5.13e-272
9	640	28.9	2933	21	Gallus gallus neururi	8.32e-195
10	215	9.7	1415	29	AB000800	4.77e-54
11	215	9.7	2549	29	Mus musculus GDNF rece	4.77e-54
12	213	9.6	2138	29	Rattus norvegicus GDNF	2.12e-53
13	213	9.6	3616	29	Rattus norvegicus RET	2.12e-53

14	210	9.5	1619	27	AF042080	Homo sapiens gila1 cel	1.14e-03
15	210	9.5	2560	28	AF038421	Homo sapiens GPR-1like	1.14e-03
16	169	7.6	1651	29	AF015172	Mus musculus GDNF rece	2.12e-05
17	166	7.5	1707	28	HS097144	Homo sapiens RET ligand	2.12e-05
18	166	7.5	2175	27	HS095847	Human GDNF receptor al	2.12e-05
19	161	7.3	1392	29	RN2072	Rattus norvegicus mRNA	1.04e-04
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23	122	5.5	1704	27	AC006095	Homo sapiens gila1 cel	2.27e-25
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45	50	2.3	154028	27	HSAC002087	Human BAC clone GS113D	3.95e-03

ALIGNMENTS

RESULT	1	LOCUS	DEFINITION	ACCESSION	NID	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE	MEDLINE	AUTHORS	TITLE	JOURNAL	FEATURES
		RN097143	Rattus norvegicus RET ligand 2 (RET12) mRNA, complete cds.	U97143	92282023		Norway rat.	Rattus norvegicus	1 (bases 1 to 2787)	Santicola, M., Hession, C.A., Worley, D.S., Carmillo, P., Eghrini, W., Walus, L., Robinson, S., Jaworski, G., Wel, H., Tizard, R., Willet, A., Pepinsky, R.B. and Cate, R.L.	Gila1 cell line-derived neurotrophic factor-dependent RET activation can be mediated by two different cell-surface proteins	Proc. Natl. Acad. Sci. U.S.A. 94 (12), 6238-6243 (1997)	97322356	2 (bases 1 to 2787)	Santicola, M., Hession, C.A., Worley, D.S., Carmillo, P., Eghrini, W., Walus, L., Robinson, S., Jaworski, G., Wel, H., Tizard, R., Willet, A., Pepinsky, R.B. and Cate, R.L.	Direct Submission	Submitted (11-APR-1997) Molecular Genetics, BIOGEN, 14 Cornhill Center, Cambridge, MA 02142, USA	1. 2787 /organism="Rattus norvegicus" /db_xref="taxon:10116" /dev_stage="embryonic" /tissue_type="brain/kidney" 1. 2787 /gene="RET12" 121. 1515 /gene="RET12"


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AUTHORS			Trupp, M., Raynoschek, C. and Ibanez, C.F.	
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REFERENCE			2 (bases 1 to 1395)	
AUTHORS			Trupp, M., Raynoschek, C. and Ibanez, C.F.	
TITLE			Direct Submision	
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ORIGIN

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Query Match	61.2%	Score 1355;	DB 29;	Length 1395;
Best Local Similarity	99.9%	Pred. No. 0.0e+00;		
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			Gaps	0;
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Qy	770	CTGGGGCCCCCAAGTGAAGTGTGTCCGGGCCCAATGAGCTGTGTGGCTGAATCCAATG	829	
Db	159	CAGCTCCAGGTACCCGACCTTTGGGAGTGTCTGGCAGGGCGGGATGGCAATACCAATG	218	
Qy	830	CAGCTCCAGGTACCCGACCTTTGGCAGTGTCTGGCAGGGCGGGATGGCAATACCAATG	889	
Db	219	GGCCATAAGGAGTGCCAGGAGCCCTGGAGGCTTTCAGAGAAAGCCACATGATGACTG	278	
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Db	279	CCGCTGCAAGGGGGGCATGAGAAAGAGACTGTCTGTGAGATCTACTGGAGATCCA	338	
Qy	950	CCGCTGCAAGGGGGGCATGAGAAAGAGACTGTCTGTGAGATCTACTGGAGATCCA	1009	
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Qy	1010	TCGTGGGCTGCAGAGGGGTGAGAGTTCTATGAGACTTCCCCATGAGCTGTGACCTC	1069	
Db	399	GGGCTCTCGGACATCTTCAGGCTTCGCTTCATCTTCTCAGAGGACAGGACAGCCGGC	458	
Qy	1070	GGGCTCTCGGACATCTTCAGGCTTCGCTTCATCTTCTCAGAGGACAGGACAGCCGGC	1129	
Db	459	AGTCAGTACCAAAAGCAACCACTGCTGTGAATGCGCCCAAGGCTGTGCAACTGATGACAA	518	
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Db	519	CTGCAAGAAGTTGGCTCTCTTATATCTCCATCTGCACACCGTAGATCTCTCCACCGA	578	
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Db	579	ACGCGCAACGGCGGCAAGTGCACAAGGCTGTGGGCAAGTTCTTGAACGTGTGGCCAG	638	
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Db	639	CGAGTATACCTACCGCATGCTCTTCTGTGCTCTGTCAAGACAGGCATGTGCTGAGCTCG	698	
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QY	1850	CCTGGGAGCAAGTGTCTATCACCACCCTCGACATCTATTCAGGAGCAAGAGGCTGAAGGCCAA	1322
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BASE COUNT 306 a 442 c 361 g 283 t
ORIGIN

Query Match 56.58; Score 1252; DB 29; Length 1392;
Best Local Similarity 96.38; Pred. No. 0.00e+00;
Matches 1302; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

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RESULT 4
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DEFINITION Homo sapiens RET ligand 2 (RET2) mRNA, complete cds.
ACCESSION U97145
NID 92282027
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2906)
AUTHORS Sanicola,M., Hession,C.A., Worley,D.S., Carmillo,P., Ehrenfels,C., Walus,L., Robinson,S., Jaworski,G., Wei,H., Tizard,R., Whitley,A., Pepinsky,R.B. and Cate,R.L.
TITLE Glial cell line-derived neurotrophic factor-dependent RET activation can be mediated by two different cell-surface accessory proteins
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (12), 6238-6243 (1997)
MEDLINE 97322356
REFERENCE 2 (bases 1 to 2906)

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 LOCUS HSU93703 1395 bp mRNA PRI 01-JUL-1997
 DEFINITION Human glial cell line-derived neurotrophic factor receptor beta
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 ACCESSION U93703
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 SOURCE Homo sapiens
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 1 (bases 1 to 1395)
 Martiovaara K., Suanto P., Horelli-Kuitunen N., Lindahl M.,
 Moshaykov M., Aliraksinen M.S., Palotie A., Sariola H. and Saarma
 M.
 Cloning, mRNA distribution and chromosomal localisation of the gene
 for the human glial cell line-derived neurotrophic factor beta, a
 homologue to GDNF-alpha
 Unpublished
 2 (bases 1 to 1395)
 Suanto P., Martiovaara K. and Saarma M.
 Direct Submission
 Submitted (06-MAR-1997) Molecular Neurobiology, Institute of
 Biotechnology, UP 56, University of Helsinki 00014, Finland
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 Query Match 50.4%; Score 116; DB 27; Length 1395;
 Best Local Similarity 90.6%; Pred. No. 0.00e+00;
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Qy	1550	TCTGGGCTCTTATGCTGAGTGAATGGGTTGATATGATGACCCCACTTAATGTGACTCAA	1609
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Qy	1610	CCCCACGGGCAATGCTGTCTCTCCCTGTGTCATTTGCTGTGCGACGTGGGACATGGAAGA	1669
Dp	970	AGATTTGCTGAAGTTTCTGAATTTTTTAAAGCAATACGTGTCTCAAAAATGCAATTA	1029
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Dp	1030	AGCCTTGGCAATGCTCGATGATGACATATGAGGACGACGCCCCCGCTGCTC	1082
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RESULT	11
LOCUS	AF014117 2549 bp mRNA ROD 20-NOV-1997
DEFINITION	Mus musculus GDNF receptor alpha (GDNFR-alpha) mRNA, complete cds
ACCESSION	AF014117
NID	92624960
KEYWORDS	.
SOURCE	house mouse.
ORGANISM	Mus musculus
	Eukaryote; Metazoa; Chordata; Vertebrate; Mammalia; Eutheria;
	Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 2549)
AUTHORS	Dey,B.K., Wong,Y.W., and Too,H.P.
TITLE	Cloning of a novel murine isoform of the glial cell line-derived neurotrophic factor receptor
JOURNAL	Neuroreport 9 (1) (1998) In press

REFERENCE	2 (bases 1 to 2549)
AUTHORS	Dey, B.K., Mong, Y.W. and Too, H.P.
TITLE	Direct Submission
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	/codon_start=1
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BASE COUNT	623 a 680 c 693 g 553 t
ORIGIN	
Query Match	9.7%: Score 215; DB 29; Length 2549;
Best Local Similarity	65.4%: Pred. No. 4,77e-54;
Matches	584; Conservative 0; Mismatches 297; Indels 12;
Db	1114 GGCAGAGATAGTGCAGCCGCTATGAGAGCCTTGACGAGAAAGTCTCTCTAA...
QY	890 GGCAMATMAGAGATGGCCAGCGCCCTGGAGGCTTTCGAGAGAAAGCCACATGAG...
Db	1174 CCGGTGCAAGGGGGGCATGAAGAAAGAAATTTGCTGGTATCTACTGAGCATGTA...
QY	950 CCGGTGCAAGGGGGGCATGAAGAAAGAGACTCAGAGTCTGAGATCTACTGAGCATCA...
Db	1234 CCAGAGCCTG-CAG--GGAAATGACTACTGGAAGATTCCCATACAGCCGGTTACAG...
QY	1010 TCTGGGCTGACAGAGSGTGAGAGTTCTATAGAGCTTCCCATATGAGCCTGTG...
Db	1291 CAGGCTGTACATATATTCCGGGAGTCCCGTTATATATACAGATGTTTTCAGCAATGCA...
QY	1070 GCGCCTCTCGGACATCTTTCAGGCTCGCTTCATCTTCCAGGACAGGACAGACAC...
Db	1351 ACACATTTCCAAAGGAAACAACCTGCCTCGATGACAGCCAGGCGCTGCACCGATGAC...
QY	1130 GGTCTGATCCAAAGAACCAACCTGCTGGATGACCGCCAGGCGCTGCACCGATGAC...
Db	1411 CTGCAAGAATACAGATCCGCTACATACCCCTGTGA-CCACCAGCA-TGTCGAAT-GA...
QY	1190 CTGCAAGAAGCTTGCTCTCTTATATCTCATCTGCACACGATGAGATCTTCCACCGA...
Db	1468 AGTCTGCAACGCGCGCAAGTCCACAAAGCCCTCAGGACAGTTCTTGACAAAGTTCCAGC...
QY	1250 ACGCTGCAACGCGCGCAAGTCCACAAAGGCTCTGCGGCAAGTTCTTGACGCTGCCAG...
Db	1528 CAGACAGCTACAGGAGATGCTTCTGTCTCTGCTGCCGGGAGTCCGCTCACCAGAGGCG...
QY	1310 CGAGTATACCTACCGCAAGCTCTTCTGTCTCTGTCAGGACACGAGCATGTGCTGAGCGTC...
Db	1588 GCGACAGACTATCGCTCTGTGTCTCTATGAGAAGAGAGAGGCGCAACTGCTGAA...
QY	1370 CCGGCAACCACTCTCTGCCAATGTGCTCTATAGAGACAGAGAGAGCCCAACTGCTTGA...
Db	1648 TCTGCAAGACTCTGCAAGACAAATTACATCTGAGATCTGCTTGACATTTTATTAC...

OY 1430 CCTGCCAGCCTGTGTCTGACAGACCCTGTCCGGTCCGACTGGCAGATTTCCACGC 1489
 DB 1708 CAACCTGCCAGCAGAGTCTGTGACAGCACTGTCTTAAGAGAGTACAGCAGACTG 1767
 OY 1490 CAACCTGCCAGCCTGTCTGACAGCACTGTCTTCCGAGCAACTACAGCAGACTG 1549
 DB 1768 CCTCTGCGCTACTGCGGAGTGTGACAGTGTGACAGTGTCTTACATGACTGACAG 1827
 OY 1550 TCTGGGCTCTATGCTGAGTGTGAGTTGATGATGACACCACTATGTGACTGCA 1609
 DB 1828 CAGC-CT--CA--GTG-TGGCCCGCTGTGCTGACATGACAGCACTGAGCAGTGG 1881
 OY 1610 CCCCAGGCGATGCTGTGCTCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1669
 DB 1882 AGATGCTGAGTGTCTGATTTTAAAGCAATGATGCTGCTGCTGCTGCTGCTGCTGCT 1941
 OY 1670 AGAGTGTGAGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1729
 DB 1942 AGCCTTTGGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1994
 OY 1730 GGCCTTTGGTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1782

RESULT 12
 LOCUS RN059486 2138 bp mRNA ROD 23-JUL-1996
 DEFINITION Rattus norvegicus GDNF receptor alpha mRNA, complete cds.
 ACCESSION U59486
 NID 91399862
 KEYWORDS
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 2138)
 AUTHORS Jing, S.-J., Wen, D., Yu, Y., Holst, P. L., Luo, Y., Fang, M., Tamir, R., Antonio, L., Hu, Z., Cupples, R., Louis, J. C., Hu, S., Altrock, B., and Fox, G. M.
 TITLE GDNF-induced activation of the ret protein tyrosine kinase is mediated by GDNF- α , a novel receptor for GDNF
 JOURNAL Cell 85 (7), 1113-1124 (1996)
 MEDLINE 96270513
 REFERENCE 2 (bases 1 to 2138)
 AUTHORS Fox, G. M., Jing, S. J., Yu, Y., Holst, P. L., Fang, M., Tamir, R., Antonio, L., Hu, Z., and Louis, J. C.
 TITLE Direct Submission
 JOURNAL Submitted (29-MAY-1996) Immunology, Amgen, Inc., Amgen Center, Thousand Oaks, CA 91320-1789, USA
 FEATURES
 source Location/Qualifiers
 1..2138
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 /db_xref="taxon:10116"
 302..1708
 /codon_start=1
 /product="GDNF receptor alpha"
 /db_xref="PID:91399863"
 /translation="MFLATLYFALPLDLMLSAEYSGDRLDCVAPDQCKEAGSCT
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 CNLDDTCKKRSAYITPCTTSMSNEVCHNRKRLKROFEDVVPKHSYGLFCSRD
 IACTERRRQTIIVPCSYEERENPCLSLDQSKTYICRSRLADFTTCOPESRSVN
 CLKENYADCLAYSLGIVTVPNTYVDSLSLVAVWCDSNGNDLECLKFLNPFK
 NTKLNAIOAFNGSDVIMWQAPVQVTTATTTATTAFRVKNPLDPLGASENIPHLV
 PCCANLQAKIKSNVSGSHLCLSDSDGKDLAASSHITTKSMAAPPSCSLSLPV
 LMTALALSLSLSLV"

CDS
 494 a 593 c 584 g 467 c
 BASE COUNT
 ORIGIN

Query Match 9.6%; Score 213; DB 29; Length 2138;
 Best Local Similarity 65.3%; Pred. No. 2, 12e-53;
 Matches 583; Conservative 0; Mismatches 298; Indels 12; Gaps 8;

DB 502 GGCAGAGTGAATGATGCTGCTGAGCCCATGAGGCTTGAAGCAGAACTCTGTACACTG 561
 OY 890 GGCAGATAGAGTGTGACAGGAGCCCTGAGAGTCTTGAGGAAAGCCACTGTATGACTG 949
 DB 562 CCGCTGCAAGCGGGGCTGAGAAAGAGAAATGTCTGCTATCTACTGAGCATGTA 621
 OY 950 CCGCTGCAAGCGGGGCTGAGAAAGAGAACTGAGTGTGCTGAGATCTACTGAGCATGTA 1009
 DB 622 CCAGAGGCTG--CAG--GGAAATGACCTCTGGAAGATTCCTGATGAGCCGGTAAAG 678
 OY 1010 TCTGGGCTGAGAGAGGAGGAGAGTGTATATAGCTTCCCTTATGAGCTGTGACTC 1069
 DB 679 CAGGTTGTCAGATATATTCGCGGAGTCCCGTTCATATCAGATGTTTCCAGCAAGTGA 738
 OY 1070 GCGCTCTGCGACATCTTCAGGCTGCTCAATCTTCAGGAGACAGGAGACCCGCG 1129
 DB 739 ACACATTTCCAAAGGAACAATGCTGCTGAGCAGCAGCAAGGCTGCACTGTGAGACAG 798
 OY 1130 GGTCACTACCAAAAGCAACCACTGCTGAGTCCGCGCAAGGCTGCACTGTGAGACAG 1189
 DB 799 CTGTAAGAAAGTACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 855
 OY 1190 CTGCAAGAGCTTGGCTCTCTATATATCTGCAATCTGCAACGCTGATCTCTCCACGGA 1249
 DB 856 GGTCTGCAACCGCGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 915
 OY 1250 AGCCTGCAACCCCGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1309
 DB 916 CAAGCAGAGCTACGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 975
 OY 1310 CGAGTATACCTACCGCATGCTCTTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1004
 DB 976 GCGACAGACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1044
 OY 1370 CCGGCAAAACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1104
 DB 1036 TCTGCAAGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1164
 OY 1430 CCGTGGCAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1224
 DB 1096 CAACCTGCCAGCAGAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1164
 OY 1490 CAACCTGCCAGCCTCTCTACCGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1224
 DB 1156 CCTCTGCGCTACTGCGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1224
 OY 1550 TCTGGGCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1284
 DB 1216 CAGC-CT--CAGCGTGG--CACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1344
 OY 1610 CCCCAGGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1404
 DB 1270 AGACGCTGGAATTTCTGAAATTTTAAAGGACAATCTGCTCAAAATAGCATTTA 1324
 OY 1670 AGAGTGTGAGAGTCTCTCAGGAGCTTCAAGAAAAACCATGCTTCCGAGAGCCATTTA 1384
 DB 1330 AGCCTTTGGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1444
 OY 1730 GGCCTTTGGTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1504
 RESULT 13
 LOCUS RN097142 3616 bp mRNA ROD 29-JUL-1997
 DEFINITION Rattus norvegicus RET ligand 1 (RET1) mRNA, complete cds.
 ACCESSION U97142
 NID 92282021
 KEYWORDS
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 3616)

 WIRELESS (TM)

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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm
 Run on: Mon Mar 8 14:31:36 1999; Maspar time 36.56 Seconds
 694,068 Million cell updates/sec
 Tabular output not generated.

Title: >US-08-866-354-40
 Description: (1,460) from US08866354.pep
 Perfect Score: 3343
 Sequence: 1 MDVFSHYDETLRLASPS.....RARLSAALPLMLTLAL 460

Scoring table: PAM 150
 Gap 11

Searched: 180763 seqs, 55169189 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: strepmb18
 1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
 9:sp_phase 10:sp_plant 11:sp_rodent 12:sp_unclassified
 13:sp_vertebrate 14:sp_virus

Statistics: Mean 47.029; Variance 73.182; scale 0.643
 Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description	Pred. No.
1	3268	97.8	464	11	GLIAL CELL LINE-DERIVE	0.00e+00
2	3131	93.7	464	4	RET LIGAND 2.	0.00e+00
3	3120	93.3	464	4	GLIAL CELL LINE-DERIVE	0.00e+00
4	1541	46.1	468	11	GDNF RECEPTOR ALPHA.	0.00e+00
5	1539	46.0	463	11	GDNF-ALPHA/TRNRI-DELT	0.00e+00
6	1523	45.6	465	4	GPI-LINKED ANCHOR PROT	0.00e+00
7	1520	45.5	463	11	GDNF RECEPTOR BETA.	0.00e+00
8	1501	44.9	460	4	RET LIGAND 1.	0.00e+00
9	1391	41.6	431	13	GFRA RECEPTOR ALPHA 4 P	0.00e+00
10	777	23.2	397	11	GLIAL CELL LINE-DERIVE	1.02e-164
11	777	23.2	397	11	GLIAL CELL LINE-DERIVE	1.02e-164
12	777	23.2	397	11	GLIAL CELL LINE-DERIVE	1.02e-164
13	708	21.2	400	4	GDNF FAMILY RECEPTOR A	1.23e-16
14	107	3.2	913	5	GDNF FAMILY RECEPTOR A	1.11e-02
15	107	3.2	1016	5	GDNF FAMILY RECEPTOR A	1.11e-02
16	107	3.2	1046	5	GDNF FAMILY RECEPTOR A	1.11e-02
17	107	3.2	1713	11	GDNF FAMILY RECEPTOR A	1.11e-02
18	105	3.1	192	5	GDNF FAMILY RECEPTOR A	1.11e-02
19	103	3.1	287	5	GDNF FAMILY RECEPTOR A	1.11e-02
20	103	3.1	939	5	GDNF FAMILY RECEPTOR A	1.11e-02

Result ID	Score	Match	Length	ID	Description	Pred. No.
21	105	3.1	2090	5	GDNF FAMILY RECEPTOR A	1.11e-02
22	105	3.1	2153	5	GDNF FAMILY RECEPTOR A	1.11e-02
23	101	3.0	460	8	GDNF FAMILY RECEPTOR A	1.11e-02
24	99	3.0	1732	11	GDNF FAMILY RECEPTOR A	1.11e-02
25	98	2.9	179	14	GDNF FAMILY RECEPTOR A	1.11e-02
26	96	2.9	201	2	GDNF FAMILY RECEPTOR A	1.11e-02
27	96	2.9	288	5	GDNF FAMILY RECEPTOR A	1.11e-02
28	97	2.9	344	2	GDNF FAMILY RECEPTOR A	1.11e-02
29	96	2.9	368	2	GDNF FAMILY RECEPTOR A	1.11e-02
30	98	2.9	430	2	GDNF FAMILY RECEPTOR A	1.11e-02
31	97	2.9	460	8	GDNF FAMILY RECEPTOR A	1.11e-02
32	98	2.9	478	6	GDNF FAMILY RECEPTOR A	1.11e-02
33	96	2.9	480	11	GDNF FAMILY RECEPTOR A	1.11e-02
34	96	2.9	4131	5	GDNF FAMILY RECEPTOR A	1.11e-02
35	93	2.8	113	14	GDNF FAMILY RECEPTOR A	1.11e-02
36	93	2.8	275	14	GDNF FAMILY RECEPTOR A	1.11e-02
37	93	2.8	302	4	GDNF FAMILY RECEPTOR A	1.11e-02
38	93	2.8	316	3	GDNF FAMILY RECEPTOR A	1.11e-02
39	92	2.8	325	14	GDNF FAMILY RECEPTOR A	1.11e-02
40	94	2.8	650	4	GDNF FAMILY RECEPTOR A	1.11e-02
41	93	2.8	722	4	GDNF FAMILY RECEPTOR A	1.11e-02
42	92	2.8	939	5	GDNF FAMILY RECEPTOR A	1.11e-02
43	93	2.8	1095	11	GDNF FAMILY RECEPTOR A	1.11e-02
44	93	2.8	3857	11	GDNF FAMILY RECEPTOR A	1.11e-02
45	94	2.8	4472	2	GDNF FAMILY RECEPTOR A	1.11e-02

ALIGNMENTS

RESULT 1
 ID 035977; PRELIMINARY: PRT: 464 AA.

AC 035977; 01-JAN-1998 (TREMELREL. 05, CREATED)
 DT 01-JAN-1998 (TREMELREL. 05, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMELREL. 08, LAST ANNOTATION UPDATE)
 DE GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR-BETA.
 GN GDNF-ALPHA/TRNRI-DELT.
 OS RATTUS NORVEGICUS (RAT).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
 SC SCINOGNATHI; MURIDAE; MURINAE; RATTUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TRUMP M., RAYNOSCHER C., IBANEZ C.F.;
 RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN/KIDNEY;
 RX MEDLINE: 97322356;
 RA SANICOLA M., HESSION C.A., WORLEY D.S., CARMILLO P., EHRENFELT S.,
 RA WALUS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,
 RA PEPINSKY R.B., CATE R.L.;
 RT "Glial cell line-derived neurotrophic factor-dependent RET activation
 can be mediated by two different cell-surface accessory proteins."
 RT PROC. NATL. ACAD. SCI. U.S.A. 94:6238-6243(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN/KIDNEY;
 RA SANICOLA M., HESSION C.A., WORLEY D.S., CARMILLO P., EHRENFELT S.,
 RA WALUS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,
 RA PEPINSKY R.B., CATE R.L.;
 RT SUBMITTED (APR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AF005226; G232252;
 DR EMBL: U97143; G2282024;
 SQ SEQUENCE 464 AA: 51668 MW: BIA2BD11 CRC32;

Query Match 97.8%; Score 3268; DB 11; Length 464;
 Best Local Similarity 99.6%; Pred. No. 0.00e+00;

Matches 451; Conservative 1; Mismatches 1; Indels 0; Gaps 0
 Db 12 FIDETLRSLAPSSLSQSGELHGMRPQVDCVRANLCAEESNCSSRYRLRQCLAGDRDNT 71
 : |||||
 QY 8 YDETLRLASPSLSQSGELHGMRPQVDCVRANLCAEESNCSSRYRLRQCLAGDRDNT 67

 WIRE (TM)

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Merch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Mar 8 14:05:53 1999; Maspar time 16.83 Seconds

Tabular output not generated.

Title: >US-08-866-354-36
 Description: (1.464) from US08866354.pep
 Perfect Score: 3386
 Sequence: 1 MILANVFCLFFFLDDTLRSL.....RAPSALTVLSVLMKLAL 464

Scoring table:
 PAM 150
 Gap 11

Searched: 74019 seqs, 26840295 residues

Post-processing: Minimum Match 08
 Listing first 45 summaries

Database: swiss-prot36
 1:swissprot

Statistics: Mean 48.016; Variance 67.910; scale 0.707

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	3372	99.6	464	1	NRTN_HUMAN NEURTURIN RECEPTOR ALP	0.00e+00
2	3203	94.6	463	1	NRTN_MOUSE NEURTURIN RECEPTOR ALP	0.00e+00
3	2686	79.3	465	1	NRTN_CHICK NEURTURIN RECEPTOR ALP	0.00e+00
4	1534	45.9	468	1	GDNF_MOUSE GDNF RECEPTOR ALPHA PR	0.00e+00
5	1527	45.1	468	1	GDNF_MOUSE GDNF RECEPTOR ALPHA PR	0.00e+00
6	1521	44.9	464	1	GDNF_MOUSE GDNF RECEPTOR ALPHA PR	0.00e+00
7	1501	44.3	469	1	GDNF_MOUSE GDNF RECEPTOR ALPHA PR	0.00e+00
8	100	3.0	462	1	EFN1_HUMAN EFENATION FACTOR TU	3.18e-02
9	103	3.0	1712	1	TGFB_RAT TGF- β 1	9.87e-03
10	97	2.9	354	1	NOV_MOUSE NOV PROTEIN HOMOLOG GR	9.98e-02
11	95	2.8	113	1	RL19_MYCTU BETA-3 ADRENERGIC RECE	2.10e-01
12	95	2.8	408	1	B3AR_HUMAN CATHESPIN B-LIKE CYSTE	8.96e-01
13	91	2.7	342	1	CYS2_HAECO CATHESPIN B-LIKE CYSTE	8.96e-01
14	91	2.7	342	1	CYS2_HAECO CATHESPIN B-LIKE CYSTE	8.96e-01
15	91	2.7	352	1	ASPF2_BLAGE ASPARTIC PROTEASE BLA	8.96e-01
16	91	2.7	427	1	MODS_YEAST TRNA ISOEANTENYLTRANSF	8.96e-01
17	91	2.7	438	1	MODS_YEAST TRNA ISOEANTENYLTRANSF	8.96e-01
18	93	2.7	452	1	EFN1_BOVIN ELONGATION FACTOR TU	4.37e-01
19	90	2.7	513	1	HDAC_MAIZE PROBABLE HISTONE DEACE	1.28e+00
20	91	2.7	521	1	GAG_SIVAG GAG POLYPROTEIN (CORE	8.96e-01
21	93	2.7	799	1	TRKA_RAT HIGH AFFINITY NERVE GR	4.37e-01
22	91	2.7	879	1	LDLR_RAT LOW-DENSITY LIPOPROTEIN	8.96e-01
23	92	2.7	1603	1	PSC_DROME POSTERIOR SEX COMBS PR	6.27e-01

24	92	2.7	2410	1	POLL_BAYM GENOME POLYPROTEIN 1 (2.50e+00
25	92	2.7	2412	1	POLL_BAYM GENOME POLYPROTEIN 1 (2.50e+00
26	88	2.6	113	1	RL19_MYCTU BETA-3 ADRENERGIC RECE	2.10e-01
27	89	2.6	302	1	UL49_VZVD TEGMENT PROTEIN (GENE	1.1e-01
28	89	2.6	354	1	FUT2_RABIT GALACTOSIDE 2-L-FUCOSY	2.50e+00
29	88	2.6	379	1	GAL7_HUMAN GALACTOSIDE 2-L-FUCOSY	2.50e+00
30	88	2.6	381	1	DBH2_MOUSE ESTRADIOL 17 BETA-DEHY	2.50e+00
31	88	2.6	418	1	B3AR_MACW B3AR-3 ADRENERGIC RECE	2.50e+00
32	88	2.6	432	1	MDHC_MAIZE MAIATE DEHYDROGENASE (2.50e+00
33	88	2.6	463	1	TIS_SALPO TYPE I RESTRICTION ENZ	2.50e+00
34	88	2.6	480	1	ADP1_XENLA MICROBIAL SERINE PROTE	2.50e+00
35	88	2.6	621	1	ASPA_AERSA PHOSPHOLIPASE A-2-ACT1	1.1e-01
36	89	2.6	646	1	PLAP_MOUSE HIGH AFFINITY NERVE GR	1.1e-01
37	89	2.6	796	1	TRKA_HUMAN HIGH AFFINITY NERVE GR	1.1e-01
38	89	2.6	808	1	VGB_HSVS LOW-DENSITY LIPOPROTEIN	1.1e-01
39	88	2.6	854	1	LDLR_YEAST SIPI PROTEIN	1.1e-01
40	88	2.6	863	1	SIPI_YEAST SIPI PROTEIN	1.1e-01
41	88	2.6	873	1	PC1_HUMAN PLASMA-CELL MEMBRANE G	1.1e-01
42	87	2.6	1115	1	PAN2_YEAST PAB-DEPENDENT POLY(A)-	1.1e-01
43	89	2.6	1408	1	SERR_DROME SERRATE PROTEIN PRECU	1.1e-01
44	89	2.6	2703	1	NORC_DROME NEUROGENIC LOCUS NORC	1.1e-01
45	88	2.6	2871	1	FBN1_BOVIN FIBRILLIN 1 PRECURSOR	1.1e-01

ALIGNMENTS

RESULT ID	1	STANDARD:	PRT:	464 AA.
AC	000451:			
DT	01-NOV-1997 (REL. 35, CREATED)			
DT	01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)			
DT	15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)			
DE	NEURTURIN RECEPTOR ALPHA PRECURSOR (NRTN-ALPHA) (NRTN-ALPHA) (TGF- β 1) (GDNF- β 1)			
DE	BETA RELATED NEURTROPHIC FACTOR RECEPTOR 2) (GDNF RECEPTOR BETA)			
GN	(GDNF- β 1)			
GN	GFR2 OR GDNFRB OR TRNR2.			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:			
OC	EUTHERIA: PRIMATES.			
OC	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 97325791.			
RA	BALOH R.H., TANSEY M.G., GOLDEN J.P., CREEDON D.J.,			
RA	HECKEROTH R.O., KECK C.L., ZIMONJIC D.B., PORESCU N.C.,			
RA	JOHNSON E.M. JR., MIERANDI J.:			
RL	NEURON 18:793-802(1997).			
CC	-1- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NRTN-INDUCED AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR. ALSO ABLE TO MEDIANE GDNF SIGNALING THROUGH THE RET TYROSINE KINASE RECEPTOR.			
CC	-1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY SIMILARITY).			
CC	-1- ALTERNATIVE PRODUCTS: A SHORT FORM IS PRODUCED BY ALTERNATIVE SPLICING IN BOTH BRAIN AND PLACENTA.			
CC	-1- SIMILARITY: BELONGS TO THE GDNF FAMILY.			
DR	EMBL: AF002700; G2145080; -			
DR	MIM: 601956; -			
KW	RECEPTOR; GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL; ALTERNATIVE SPLICING.			
KW	SIGNAL			
FT	CHAIN	22	444	POTENTIAL.
FT	PROPEP	445	464	TGF- β 1 RELATED NEURTROPHIC FACTOR RECEPTOR 2.
FT	CARBOHYD	52	52	HYDROPHOBIC, REMOVED DURING MATURATION (POTENTIAL).
FT	CARBOHYD	357	357	POTENTIAL.
FT	CARBOHYD	413	413	POTENTIAL.
FT	LIPID	444	444	GPI-ANCHOR (POTENTIAL).
FT	VARSPLIC	14	146	MISSING (IN SHORT FORM).
SEQ	SEQUENCE	464 AA:	51558 MW:	3C74ABFB CRC32:

Query Match 99.6%; Score 3372; DB 1; Length 464;
 Best Local Similarity 99.4%; Pred. No. 0.00e+00;

Matches 461: Conservative 2: Mismatches 1: Indels 0: Gaps 0:

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Db 1 MILANVCLFFELDTLSRLSPSSLOGPELHGMRPPVDCVANELCAESNCSSRYRTL 60
Oy 1 MILANVCLFFELDTLSRLSPSSLOGPELHGMRPPVDCVANELCAESNCSSRYRTL 60
Db 61 ROCLAGDRNTMLANKCOALEVLOESPLYDCRCRGMKKELOCLQIYWSIHGLTGE 120
Oy 61 ROCLAGDRNTMLANKCOALEVLOESPLYDCRCRGMKKELOCLQIYWSIHGLTGE 120
Db 121 EYFASPEPYTSRLSDIFRLASIFSGTGADPVVSAKSNHCLDAKCNLNDCKRLSS 180
Oy 121 EYFASPEPYTSRLSDIFRLASIFSGTGADPVVSAKSNHCLDAKCNLNDCKRLSS 180
Db 181 YISICNREISPTERCNRRKCHALROFDRVPSEYTYRMLFSCQDQACAEERRQTIIPS 240
Oy 181 YISICNREISPTERCNRRKCHALROFDRVPSEYTYRMLFSCQDQACAEERRQTIIPS 240
Db 241 CSYEDKEPNCLDLRGVCRTHLCRSRLADFHANCRASTYQVTSPPADNYOACLSYAGM 300
Oy 241 CSYEDKEPNCLDLRGVCRTHLCRSRLADFHANCRASTYQVTSPPADNYOACLSYAGM 300
Db 301 IGFDMPVYVDSPTGIYVSPWCSCRGSGNNEECEFLEDFENPCLRNALQAFNGTN 360
Oy 301 IGFDMPVYVDSPTGIYVSPWCSCRGSGNNEECEFLEDFENPCLRNALQAFNGTN 360
Db 361 VVNSPKGPTFSQATAPRVEKTPSLPDDLSSTLSGTSTVITTCSTVOEGKANKSKELSM 420
Oy 361 VVNSPKGPTFSQATAPRVEKTPSLPDDLSSTLSGTSTVITTCSTVOEGKANKSKELSM 420
Db 421 CFTELTTNIPGSKVKIKPNSGSPRAPSALTIVLSVLMKLA 464
Oy 421 CFTELTTNIPGSKVKIKPNSGSPRAPSALTIVLSVLMKLA 464

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RESULT 2
ID NRTR_MOUSE STANDARD: PRT: 463 AA.

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AC 008842:
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE NEURTURIN RECEPTOR ALPHA PRECURSOR (NTRN-ALPHA) (NTRN-ALPHA) (TGF-
DE BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 2) (GDNF RECEPTOR BETA)
DE (GDNF-BETA).
GN GFR2 OR GDNFRB OR TRNR2.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN (1)
RN SEQUENCE FROM N.A.
RX MEDLINE: 97325791.
RA BALOH R.H., TANSEY M.G., GOLDEN J.P., CREEDON D.J.,
RA HEICKENROTH R.O., KECK C.L., ZIMONJIC D.B., POPESCU N.C.,
RA JOHNSON E.M., JR., MTLBRANDT J.;
RL NEURON 18:793-802(1997).
CC -1- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NTRN-INDUCED
CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR. ALSO ABLE
CC TO MEDIANE GDNF SIGNALING THROUGH THE RET TYROSINE KINASE
CC RECEPTOR.
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
CC SIMILARITY).
CC -1- TISSUE SPECIFICITY: NEURONS OF THE SUPERIOR CERVICAL AND DORSAL
CC ROOT GANGLIA, AND ADULT BRAIN AND TESTIS. LOW LEVEL IN THE SPLEEN
CC AND IN THE ADRENAL.
CC -1- ALTERNATIVE PRODUCTS: A SHORT FORM IS PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- SIMILARITY: BELONGS TO THE GDNF FAMILY.
DR EMBL: AF002701; G2145082; -.
DR MGI: MGI:1195462; GFR2.
KW RECEPTOR; GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL;
KW ALTERNATIVE SPLICING.
FT SIGNAL 1 21
FT CHAIN 22 443 TGF-BETA RELATED NEUROTROPHIC FACTOR

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FT PROPEP 444 463 RECEPTOR 2.
FT CARBOHYD 52 52 HYDROPHOBIC, REMOVED DURING MATURATION.
FT CARBOHYD 357 357 (POTENTIAL).
FT CARBOHYD 413 413 (POTENTIAL).
FT LIPID 443 413 POTENTIAL.
FT VASPLICE 14 14 GPI-ANCHOR (POTENTIAL).
SQ SEQUENCE 463 AA; 51598 MW; 0A2165C0 CRC32; MISSING (IN SHORT FORM).

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Query Match 94.6%; Score 3203; DB 1; Length 463;
Best Local Similarity 93.5%; Pred. No. 0.00e+00;
Matches 433; Conservative 19; Mismatches 11; Indels 0; Gaps

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Db 1 MILANVCLFFELDTLSRLSPSSLOGPELHGMRPPVDCVANELCAESNCSSRYRTL 60
Oy 1 MILANVCLFFELDTLSRLSPSSLOGPELHGMRPPVDCVANELCAESNCSSRYRTL 60
Db 61 ROCLAGDRNTMLANKCOALEVLOESPLYDCRCRGMKKELOCLQIYWSIHGLTGE 120
Oy 61 ROCLAGDRNTMLANKCOALEVLOESPLYDCRCRGMKKELOCLQIYWSIHGLTGE 120
Db 121 EYFASPEPYTSRLSDIFRLASIFSGTGADPVVSAKSNHCLDAKCNLNDCKRLSS 180
Oy 121 EYFASPEPYTSRLSDIFRLASIFSGTGADPVVSAKSNHCLDAKCNLNDCKRLSS 180
Db 181 YISICNREISPTERCNRRKCHALROFDRVPSEYTYRMLFSCQDQACAEERRQTIIPS 240
Oy 181 YISICNREISPTERCNRRKCHALROFDRVPSEYTYRMLFSCQDQACAEERRQTIIPS 240
Db 241 CSYEDKEPNCLDLRGVCRTHLCRSRLADFHANCRASTYQVTSPPADNYOACLSYAGM 300
Oy 241 CSYEDKEPNCLDLRGVCRTHLCRSRLADFHANCRASTYQVTSPPADNYOACLSYAGM 300
Db 301 IGFDMPVYVDSPTGIYVSPWCSCRGSGNNEECEFLEDFENPCLRNALQAFNGTN 360
Oy 301 IGFDMPVYVDSPTGIYVSPWCSCRGSGNNEECEFLEDFENPCLRNALQAFNGTN 360
Db 361 VVNSPKGPTFSQATAPRVEKTPSLPDDLSSTLSGTSTVITTCSTVOEGKANKSKELSM 420
Oy 361 VVNSPKGPTFSQATAPRVEKTPSLPDDLSSTLSGTSTVITTCSTVOEGKANKSKELSM 420
Db 421 CFTELTTNIPGSKVKIKLYSGCRARLSTALPILMVTLA 463
Oy 421 CFTELTTNIPGSKVKIKPNSGSPRAPSALTIVLSVLMKLA 463

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RESULT 3
ID NRTR_CHICK STANDARD: PRT: 465 AA.

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AC 013157:
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE NEURTURIN RECEPTOR ALPHA PRECURSOR (NTRN-ALPHA) (NTRN-ALPHA) (GDNF
DE RECEPTOR BETA) (GDNF-BETA).
GN GFR2 OR GDNFRB.
OS GALLUS GALLUS (CHICKEN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
OC GALLIFORMES.
RN [1]
RN SEQUENCE FROM N.A.
RX TISSUE-BRAIN.
RA ROSENTHAL A., CHINCHETRU M., BUCHMAN V.L., DAVIES A.M.;
RL NATURE 387:721-724(1997).
CC -1- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NTRN-INDUCED
CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR. ALSO ABLE
CC TO MEDIANE GDNF SIGNALING THROUGH THE RET TYROSINE KINASE
CC RECEPTOR (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.
CC -1- SIMILARITY: BELONGS TO THE GDNF FAMILY.
DR EMBL: U90542; G221805; -.
KW RECEPTOR; GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL.

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FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 445 NEUTURIN RECEPTOR ALPHA.
FT PROPEP 446 465 HYDROPHOBIC, REMOVED DURING MATURATION
(POTENTIAL).
FT CARBOHYD 355 355 POTENTIAL.
FT CARBOHYD 387 387 POTENTIAL.
FT CARBOHYD 412 412 POTENTIAL.
FT LIPID 445 445 GPI-ANCHOR (POTENTIAL).
SQ SEQUENCE 465 AA: 51908 MW: 5CA073E4 CRC32:

Query Match 79.3% Score 2686; DB 1; Length 465;
Best Local Similarity 74.7% Pred. No. 0.00e+00;
Matches 349; Conservative 70; Mismatches 43; Indels 5; Gaps 3;

Db 1 MILANAFVLEVDLTLAAPPSPGODLOGNRPVDCIANTLCAEGSCSRRTYL 60
QY 1 MILANVCLFFLDLTLASPSLOPELHGRPPVDCYANLCAAESNCSSRYTL 60
Db 61 RQCLAGDRNTMLANKECQALAEVLQESPLYDCRCRGRMKREIOQYVWSIHGLAGE 120
QY 61 RQCLAGDRNTMLANKECQALAEVLQESPLYDCRCRGRMKREIOQYVWSIHGLAGE 120
Db 121 EFYEASPEYPTSRSLDIFRLASTISG--DPATNSKNHCLDAKACNLNCKRLSG 178
QY 121 EFYEASPEYPTSRSLDIFRLASTISG--DPATNSKNHCLDAKACNLNCKRLSG 178
Db 121 EFYEASPEYPTSRSLDIFRLASTISG--DPATNSKNHCLDAKACNLNCKRLSG 178
QY 121 EFYEASPEYPTSRSLDIFRLASTISG--DPATNSKNHCLDAKACNLNCKRLSG 178
Db 179 YISTCKEISATEHCRRKCHALROFDPNVPSEYTYRLFCSCDKOQACPRROTIVF 238
QY 179 YISTCKEISATEHCRRKCHALROFDPNVPSEYTYRLFCSCDKOQACPRROTIVF 238
Db 181 YISICNREISPTERCNRKCHALROFDPNVPSEYTYRLFCSCDKOQACPRROTIVF 240
QY 181 YISICNREISPTERCNRKCHALROFDPNVPSEYTYRLFCSCDKOQACPRROTIVF 240
Db 239 CSYEDKERNCLDLRNVCRAHDLCSRSLADFHANCOASFOSLSCPGDNYOACLSYTL 298
QY 239 CSYEDKERNCLDLRNVCRAHDLCSRSLADFHANCOASFOSLSCPGDNYOACLSYTL 298
Db 241 CSYEDKERNCLDLRNVCRAHDLCSRSLADFHANCOASFOSLSCPGDNYOACLSYTL 300
QY 241 CSYEDKERNCLDLRNVCRAHDLCSRSLADFHANCOASFOSLSCPGDNYOACLSYTL 300
Db 299 IGFDMTRVYVASTSITISPCSCSGNLEEECEKRLPOTEMPCRLNIAQAGNTD 358
QY 299 IGFDMTRVYVASTSITISPCSCSGNLEEECEKRLPOTEMPCRLNIAQAGNTD 358
Db 301 IGFDMTRVYVASTSITISPCSCSGNLEEECEKRLPOTEMPCRLNIAQAGNTD 360
QY 301 IGFDMTRVYVASTSITISPCSCSGNLEEECEKRLPOTEMPCRLNIAQAGNTD 360
Db 359 VNLSPKNSPTITMLPKVEKSPALPDINDSNVMTDTSITTCISIOEHGOKLNKSKOS 418
QY 359 VNLSPKNSPTITMLPKVEKSPALPDINDSNVMTDTSITTCISIOEHGOKLNKSKOS 418
Db 361 VNLSPKNSPTITMLPKVEKSPALPDINDSNVMTDTSITTCISIOEHGOKLNKSKOS 419
QY 361 VNLSPKNSPTITMLPKVEKSPALPDINDSNVMTDTSITTCISIOEHGOKLNKSKOS 419
Db 419 LCYSETQITDTMDQKTFVDOKAAGSRHARILPAVPIVLKLL 465
QY 419 LCYSETQITDTMDQKTFVDOKAAGSRHARILPAVPIVLKLL 465
Db 420 MCFTE--LTNIIIPGSKVYIKRNSGSRARPAALTVSLMLKAL 464
QY 420 MCFTE--LTNIIIPGSKVYIKRNSGSRARPAALTVSLMLKAL 464

RESULT 4
ID GDNF_RAT STANDARD; PRT; 468 AA.
AC 062997;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DE GDNF RECEPTOR ALPHA PRECURSOR (GDNF-ALPHA) (GDF-BETA RELATED
NEUROTROPIC FACTOR RECEPTOR 1) (RET LIGAND 1).
GN GFRAL OR GDNFRA OR TRNRI OR RETL.
OS RATTUS NORVEGICUS (RAT).
CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
CC EUHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-RETINA.
RX MEDLINE: 96270513.
RA JING S., WEN D., YU Y., HOLST P.L., LYO Y., FANG M., TAMIR R.,
ANTONIO L., HU Z., CUPPLES R., LOUIS J.-C., HU S., ALTHROCK B.W.,
FOX G.M.;
RA CELL 85:1113-1124(1996).
RL [2]
RN SEQUENCE FROM N.A.
RP STRAIN-MISTAR; TISSUE-KIDNEY;
RX MEDLINE: 97322356.
RA SANICOLA M., HESSION C.A., WORLEY D.S., CARMILLO P., EHRENFELS C.,
MALUS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,

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DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF-BETA RELATED)
 DE NEUROTRONIC FACTOR RECEPTOR 1).
 GN GFRAL OR GDNFR OR TRNR1.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE-DORSAL ROOT GANGLION;
 RA WATABE K.;
 RL SUBMITTED (FEB-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED
 CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR (BY
 CC SIMILARITY).
 CC -1- SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE THOUGHT TO FORM A COMPLEX
 CC WITH THE DISULFIDE-LINKED GDNF DIMER AND WITH 2 MOLECULES OF RET
 CC (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.
 DR EMBL: AB000800; G3816442; -
 DR MGD: MGI:1100842; GFRAL
 KM RECEPTOR; GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL.
 FT SIGNAL 1 24
 FT CHAIN 25 430 GDNF RECEPTOR ALPHA.
 FT PROPEP 431 468 HYDROPHOBIC, REMOVED DURING MATURATION
 FT DOMAIN 362 369 THR-RICH.
 FT CARBOHYD 59 59 POTENTIAL.
 FT CARBOHYD 347 347 POTENTIAL.
 FT CARBOHYD 406 406 POTENTIAL.
 FT LIPID 430 430 GPI-ANCHOR (POTENTIAL).
 SQ SEQUENCE 468 AA; 51782 MW; 6C64C182 CRC32;
 Query Match 45.18; Score 1527; DB 1; Length 468;
 Best Local Similarity 48.18; Pred. No. 0.00e+00;
 Matches 216; Conservative 104; Mismatches 111; Indels 18; Gaps 15;
 Db 16 LMSAEVSG-GDRLDVCVASDOCLKEOSCTKYRTLRCQVAGKTFNLSGLBAKDECRS 74
 Qy 26 LQPELHGRMPYDCVRANELCAESNCSRYTLRQCLAGRORNTM--LANK-ECQA 80
 Db 75 AMEALOKSLYNCRCRGMKKEKNCRLIYWSMTOST-OGNDLLEDSPEYVNSRLSDIFR 133
 Qy 81 ALBVLQESPLYDCRCRGMKKEKNCRLIYWSMTOST-OGNDLLEDSPEYVNSRLSDIFR 140
 Db 134 AVFPIIDVFOQVEHISGNCLDAKACNLDIPCKRYRKYITPCTTSMN-NEVCNRRC 192
 Qy 141 LAFISGTGADPVVSAKSNHCLDAKACNLDNCKRKLRSYISICNRELSPTERCNRRC 200
 Db 193 HKALROFFDVKPAKHSYGMFLCSCRDACTERRRROTIVPVSSEBRPNCNLNODSCKT 252
 Qy 201 HKALROFFDVKPAKHSYGMFLCSCRDACTERRRROTIVPVSSEBRPNCNLNODSCKT 260
 Db 253 NYICRSLADFTNCOPEHSVSNCLKENYADCLLAYSGLIGVTMPNTYIDS-S-LSYA 310
 Qy 261 DHCRLSLADFTNCOPEHSVSNCLKENYADCLLAYSGLIGVTMPNTYIDS-S-LSYA 320
 Db 311 PMDCDSNGNDEDLCKLNFEDKNTCLKNAIAFGNGSVYTMOPAPPVQTTAMTTA 370
 Qy 321 PMDCDSNGNDEDLCKLNFEDKNTCLKNAIAFGNGSVYTMOPAPPVQTTAMTTA 379
 Db 371 FRICNPLGPAKSENEIPTHVLPKCANLQAKLSNVSSTHCLSDNDYGRKGLGASS 430
 Qy 380 -KTPSLPDLSST-S-LGTSYITTCISVQEGKANKSKLSMCFE--LTTNIIIPGSNK 435
 Db 431 HITTKS-MA-APPSGLSLPLVAVFTALA 457
 Qy 436 VIKPNSGPRARPSALTYLSVLMK-LA 463
 RESULT 6

ID GDNF_HUMAN STANDARD; PRT: 464 AA.
 AC P56159;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF-BETA RELATED)
 DE NEUROTRONIC FACTOR RECEPTOR 1).
 GN GFRAL OR GDNFR OR TRNR1.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE-SUBSTANTIA NIGRA;
 RX MEDLINE; 96270513.
 RA JING S., WEN D., YU Y., HOLST P.L., LUO Y., FANG M., TAMR R.,
 RA ANTONIO L., HU Z., CUPPLES R., LOUIS J.-C., HU S., ALTHROCK B.W.,
 RA FOX G.M.;
 RL CELL 85:1113-1124(1996).
 CC -1- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED
 CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR (BY
 CC SIMILARITY).
 CC -1- SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE THOUGHT TO FORM A COMPLEX
 CC WITH THE DISULFIDE-LINKED GDNF DIMER AND 2 MOLECULES OF RET (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.
 DR MIM: 601496; -
 KM RECEPTOR; GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL.
 FT SIGNAL 1 24
 FT CHAIN 25 428 GDNF RECEPTOR ALPHA.
 FT PROPEP 429 464 HYDROPHOBIC, REMOVED DURING MATURATION
 FT DOMAIN 361 368 POLY-THR.
 FT CARBOHYD 59 59 POTENTIAL.
 FT CARBOHYD 346 346 POTENTIAL.
 FT CARBOHYD 405 405 POTENTIAL.
 FT LIPID 428 428 GPI-ANCHOR (POTENTIAL).
 SQ SEQUENCE 464 AA; 51291 MW; 2C8C3574 CRC32;
 Query Match 44.98; Score 1521; DB 1; Length 464;
 Best Local Similarity 48.38; Pred. No. 0.00e+00;
 Matches 223; Conservative 100; Mismatches 121; Indels 18; Gaps 15;
 Db 2 FLATLFAFLPLDLILSAEVS-GDRLDVCVASDOCLKEOSCTKYRTLRCQVAGKTFNLSGLBAKDECRS 74
 Qy 12 FLDTITRSLASFSLLQPELHGRMPYDCVRANELCAESNCSRYTLRQCLAGRORNTM--LANK-ECQA 80
 Db 61 SLASGLBAKDECRSAMEALOKSLYNCRCRGMKKEKNCRLIYWSMTOST-OGNDLLEDSPEYVNSRLSDIFR 133
 Qy 71 TM--LANK-ECQAALBVLQESPLYDCRCRGMKKEKNCRLIYWSMTOST-OGNDLLEDSPEYVNSRLSDIFR 140
 Db 120 PREPNVNSRLSDIFRVAFFISDVFOVEHLPKNNCLDAKACNLDIPCKRYRKYITPCTTSMN-NEVCNRRC 192
 Qy 127 PREPNVNSRLSDIFRVAFFISDVFOVEHLPKNNCLDAKACNLDIPCKRYRKYITPCTTSMN-NEVCNRRC 200
 Db 180 TSVS-NDVCNRRCRKALROFFDVKPAKHSYGMFLCSCRDACTERRRROTIVPVSSEBRPNCNLNODSCKT 252
 Qy 187 REISPTERCNRRCRKALROFFDVKPAKHSYGMFLCSCRDACTERRRROTIVPVSSEBRPNCNLNODSCKT 260
 Db 239 EXPNCL-LDQSKTYNCRSLADFTNCOPEHSVSNCLKENYADCLLAYSGLIGVTMPNTYIDS-S-LSYA 310
 Qy 247 EXPNCL-LDQSKTYNCRSLADFTNCOPEHSVSNCLKENYADCLLAYSGLIGVTMPNTYIDS-S-LSYA 320
 Db 298 PNTYIDS-S-LSYAPMDCDSNGNDEDLCKLNFEDKNTCLKNAIAFGNGSVYTMOPAPPVQTTAMTTA 379
 Qy 307 PNTYIDS-S-LSYAPMDCDSNGNDEDLCKLNFEDKNTCLKNAIAFGNGSVYTMOPAPPVQTTAMTTA 379
 Db 356 APPVQTTAMTTATLRYKKNPLGPAKSENEIPTHVLPKCANLQAKLSNVSSTHCLSDNDYGRKGLGASS 430
 Qy 367 GPSFOATQAPRV-E-KTPSLPDLSST-S-LGTSYITTCISVQEGKANKSKLSMCFE--LTTNIIIPGSNK 435
 RESULT 6

Db	416	NGNRECEGLASSHITTKS-NA-APPSGSLPILVLT-AA	454
Oy <td>424</td> <td>ELTNIIP-GSNKVIKRNPSGRAPRAPSALIVLSYMLKIAL</td> <td>464</td>	424	ELTNIIP-GSNKVIKRNPSGRAPRAPSALIVLSYMLKIAL	464
RESULT	7	STANDARD:	PRT: 469 AA.
ID	GNDR.CHICK	013156:	
AC	01-NOV-1997	(REL. 35, CREATED)	
DT	01-NOV-1997	(REL. 35, LAST SEQUENCE UPDATE)	
DT	15-JUL-1998	(REL. 36, LAST ANNOTATION UPDATE)	
DE	GNDR RECEPTOR ALPHA PRECURSOR (GNDR-ALPHA)	(TGF-BETA RELATED	
DE	NEUROTHORPHIC FACTOR RECEPTOR 1).		
GN	GNDRAL OR GNDRFA.		
OS	GALLUS GALLUS (CHICKEN).		
OC	EDUAROTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPLATA: AVES; NEOGNATHAE;		
OC	GALLIFORMES.		
RP	[1]		
RC	SEQUENCE FROM N.A.		
RC	TISSUE-BRAIN.		
RA	BUU-BELLO A., ADU J., PINON L.G.P., HORTON A., THOMPSON J.,		
RA	ROSENTHAL A., CHINCHEIRO M., BUCHMAN V.L., DAVIES A.M.;		
RL	NATURE 387:721-724(1997).		
CC	-1- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED		
CC	AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR (BY		
CC	STIMULARITY).		
CC	-1- SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE THOUGHT TO FORM A COMPLEX		
CC	WITH THE DISULFIDE-LINKED GDNF DIMER AND WITH 2 MOLECULES OF RET		
CC	(BY STIMULARITY).		
CC	-1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY		
CC	STIMULARITY).		
CC	-1- STIMULARITY: BELONGS TO THE GDNFR FAMILY.		
DR	EMBL: U90541; G2213803; -		
KW	RECEPTOR: GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL.		
FT	SIGNAL	1	27
FT	CHAIN	28	430
FT	PROPEP	431	469
FT			
FT	DOMAIN	361	368
FT	CARBOHYD	62	62
FT	CARBOHYD	163	163
FT	CARBOHYD	346	346
FT	CARBOHYD	405	405
FT	LIPID	430	430
SO	SEQUENCE	469 AA; 52043 MW; C8D241C9 CRC32;	
Query Match	44.3%;	Score 1501;	DB 1; Length 469;
Best Local Similarity	50.7%;	Pred. No. 0.00e+00;	
Matches	224; Conservative	92; Mismatches 101; Indels	25; Gaps 18;
Db	30	LDCVNASDOCKEKSOCSTKRYRTLRCQVAGKSNFSRATGLBAKDECKSAMALOKSLYN	89
Oy	38	VDCVRANLCLCAESKSSRYRTLQCLAGR-----RNTMLANK-ECQAALEVLQESLDY	92
Db	90	CRCKRGKMKKCNLCRIIYMSYQSL-QGNDLLEDSPEYEVNSRLSDIFRLAIVS--VEP	145
Oy	93	CRCKRGKMKKELQCLQIYMSIHGLGTEGEFEYASPYEPTVSRSLDIFRLASIFSGTADP	152
Db	146	VLS-KGNCCDAACACNLNDCKRFRSAIYIPCCSSIS-NIICKKRCRCHALRLEFDKVP	203
Oy	153	VVASNSNCCDAACACNLNDCKKLRSSYISICRREISPFERCNRRKCHKALRQFEDRPV	212
Db	204	PKHSGYMGFCSCRDVACTERRRRTIVPVCSEYDEKRPCLMIQESCKKNYICRSRLADF	263
Oy	213	SEYTRMLFCCGQODQERRRRTIILPSCSEYDEKRPCLDLRQVCRDHLICRRLDFH	272
Db	264	TNCPDESSVSCKLENTADCLLAYSGLIGVTMPNTYIDS-S-LSYAPWCDCSNGNDI	321
Oy	273	ANCRASYOTVITSCPADNTQACLGSAAGMIGCDMPNIVYDSSPTIIVSPMCSCGSGNME	332
Db	322	DECRFLNFPDQNTCLKNAIAFGNGCDVYVNWOPILPVQTTATT--TASLTKNTGSETT	380
Oy	333	EECEKFLKDFENPCPLRNAIAQFNGVIVNWSYPKGPSQAQAPARVEKTPSLPDDLS DST	392

ID	RESULT	8	STANDARD	PRT	452 AA.
Db	381	NNPETHNDSPACNNLQAOKKRKNSEVDDELCLNENAIKGDNTPGVSTSHISENSFAL	440		
Qy	333	S--LGT-SVITTCISVQBOGL-KANNSEKLSMCTTE--LTTNIITPG-SNRVIRP-NS-G-442			
Db	441	PTSEFYPSTPLILMTI-ALSLFL	461		
Qy	443	PSRAPSPALVLSVLMKLAL	464		
AC	PA9411				
DT	01-FEB-1996	(REL. 33, CREATED)			
DT	01-OCT-1996	(REL. 33, LAST SEQUENCE UPDATE)			
DT	13-JUL-1998	(REL. 36, LAST ANNOTATION UPDATE)			
DE	ELONGATION FACTOR TU, MITOCHONDRIAL PRECURSOR (P43).				
GN	TUFM.				
OS	HOMO SAPIENS (HUMAN).				
OC	EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:				
OC	EUTHERIA: PRIMATES.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-LIVER;				
RC	MEDLINE: 96138557.				
RA	MORIAX V.L., BURKHART W.A., SPREMUILLI L.L.;				
RL	BIOCHIM. BIOPHYS. ACTA 1264:347-356(1995).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-KIDNEY, AND HEART;				
RC	MEDLINE: 97473528.				
RA	LING M., MERANTE F., CHEN H.-S., DUFE C., DUNCAN A.M.V.,				
RA	ROBINSON B.H.;				
RL	GENE 197:325-336(1997).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-LIVER;				
RC	MEDLINE: 95129693.				
RA	WELLS J., HENKLER F., LEVERSHA M., KOSHY R.;				
RL	FEBS LETT. 358:119-125(1995).				
RN	[4]				
RP	PARTIAL SEQUENCE OF 44-54.				
RC	TISSUE-HEART;				
RC	DUNN M.J.;				
RA	SUBMITTED (MAR-1996) TO THE SWISS-PROT DATA BANK.				
RL	-1- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF				
CC	AMINOACID-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN				
CC	BIOSYNTHESIS.				
CC	-1- SUBCELLULAR LOCATION: MITOCHONDRIAL.				
CC	EMBL: X38995; G704416; -.				
DR	EMBL: X84694; G899285; -.				
DR	EMBL: S75463; G833999; ALT_INIT.				
DR	HSC-ZDPAGE; P49411; HUMAN.				
DR	MIM: 602389; -.				
KW	PROSITE: PS00301; EFACFOR_GTP: 1.				
KW	ELONGATION FACTOR: PROTEIN BIOSYNTHESIS; MITOCHONDRION;				
KW	TRANSIT PEPTIDE; GTP-BINDING.				
FT	TRANSIT	1	43		
FT	CHAIN	44	452		
FT	NP_BIND	64	71		
FT	NP_BIND	126	130		
FT	NP_BIND	181	184		
FT	CONFLICT	195	197		
FT	CONFLICT	384	384		
SO	SEQUENCE	452 AA;	49541 MW;	F29C73C5 CRC32;	
Db	231	LGIKSVQKLLDAVDTIYPVPAKDLEKFLPLVEAVSVSPRGIVYVGTLEKGLKKDEC	230		
Qy	114	LGLTGEDEEYFA-SPEYEWVS-LSDFIRLA-SIFGAGADPVVSKSNH-CIDAKKAC	168		

DB 291 ELLGSKNRTVTGTI 306
OY 169 NLNDCKKLRSSYISI 184

RESULT 9
ID TGF β -RAT STANDARD: PRT: 1712 AA.

AC 000918;
DT 01-JUL-1993 (REL. 26, CREATED)
DT 01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR
DE (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-
GN 1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT).
OS RATTUS NORVEGICUS (RAT).
OC EUTHERIA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; MAMMALIA.
RN
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX TSUJI T., OKADA F., YAMAGUCHI K., NAKAMURA T.;
RA PROC. NATL. ACAD. SCI. U.S.A. 87:8835-8839(1990).
CC -1- SUBUNIT: THE LARGE LATENT COMPLEX OF TGF-BETA1 FROM PLATELETS IS
CC COMPOSED OF THE TGF-BETA1 MOLECULE NONCOVALENTLY ASSOCIATED WITH
CC A MASKING PROTEIN CONSISTING OF A DISULFIDE-BONDED COMPLEX OF A
CC DIMER OF THE N-TERMINAL PROPEPTIDE OF THE TGF-BETA1 PRECURSOR AND
CC A THIRD COMPONENT DENOTED TGF-BETA1-BP (OR MP LARGE SUBUNIT).
CC TGF-BETA1-BP DOES NOT BIND DIRECTLY TO ACTIVE TGF-BETA1.
CC -1- SIMILARITY: CONTAINS 18 EGF-LIKE DOMAINS.
CC EMBL: M55431; G207286;
DR DR HSSP: P19398; LATA.
DR DR PROSITE: PS00010; ASX_HYDROXYL; 13.
DR DR PROSITE: PS00022; EGF_1; 2.
DR DR PROSITE: PS01186; EGF_2; 10.
DR DR PROSITE: PS01187; EGF_CA; 15.
KW GROWTH FACTOR BINDING; REPEAT; EGF-LIKE DOMAIN; HYDROXYLATION; SIGNAL.
FT SIGNAL 1 20
FT PROPEP 21 736
FT CHAIN 737 1577
FT SITE 734 736
FT SITE 1575 1577
FT PROPEP 1578 1712
FT DOMAIN 181 213
FT DOMAIN 391 423
FT DOMAIN 531 604
FT REPEAT 618 658
FT DOMAIN 671 721
FT REPEAT 721 761
FT DOMAIN 761 865
FT DOMAIN 865 906
FT DOMAIN 907 948
FT DOMAIN 949 989
FT DOMAIN 990 1029
FT DOMAIN 1030 1070
FT DOMAIN 1071 1111
FT DOMAIN 1112 1152
FT DOMAIN 1153 1193
FT DOMAIN 1194 1235
FT DOMAIN 1236 1277
FT DOMAIN 1278 1320
FT REPEAT 1340 1392
FT REPEAT 1415 1457
FT DOMAIN 1458 1498
FT REPEAT 1517 1568
FT DOMAIN 1569 1612
FT DOMAIN 1613 1652
FT DOMAIN 1653 1697
FT DISULFID 185 195
FT DISULFID 189 201
FT DISULFID 203 212
FT DISULFID 395 405
FT DISULFID 399 411

FT DISULFID 413 422 BY SIMILARITY.
FT DISULFID 622 633 BY SIMILARITY.
FT DISULFID 638 642 BY SIMILARITY.
FT DISULFID 644 657 BY SIMILARITY.
FT DISULFID 869 881 BY SIMILARITY.
FT DISULFID 876 890 BY SIMILARITY.
FT DISULFID 892 905 BY SIMILARITY.
FT DISULFID 911 923 BY SIMILARITY.
FT DISULFID 918 932 BY SIMILARITY.
FT DISULFID 934 947 BY SIMILARITY.
FT DISULFID 953 964 BY SIMILARITY.
FT DISULFID 959 973 BY SIMILARITY.
FT DISULFID 976 988 BY SIMILARITY.
FT DISULFID 994 1005 BY SIMILARITY.
FT DISULFID 1000 1014 BY SIMILARITY.
FT DISULFID 1017 1028 BY SIMILARITY.
FT DISULFID 1034 1045 BY SIMILARITY.
FT DISULFID 1046 1054 BY SIMILARITY.
FT DISULFID 1056 1069 BY SIMILARITY.
FT DISULFID 1075 1086 BY SIMILARITY.
FT DISULFID 1081 1095 BY SIMILARITY.
FT DISULFID 1097 1110 BY SIMILARITY.
FT DISULFID 1116 1127 BY SIMILARITY.
FT DISULFID 1132 1136 BY SIMILARITY.
FT DISULFID 1138 1151 BY SIMILARITY.
FT DISULFID 1157 1169 BY SIMILARITY.
FT DISULFID 1164 1178 BY SIMILARITY.
FT DISULFID 1180 1192 BY SIMILARITY.
FT DISULFID 1198 1210 BY SIMILARITY.
FT DISULFID 1204 1219 BY SIMILARITY.
FT DISULFID 1221 1234 BY SIMILARITY.
FT DISULFID 1240 1252 BY SIMILARITY.
FT DISULFID 1246 1261 BY SIMILARITY.
FT DISULFID 1263 1276 BY SIMILARITY.
FT DISULFID 1282 1294 BY SIMILARITY.
FT DISULFID 1289 1303 BY SIMILARITY.
FT DISULFID 1305 1319 BY SIMILARITY.
FT DISULFID 1419 1432 BY SIMILARITY.
FT DISULFID 1441 1456 BY SIMILARITY.
FT DISULFID 1443 1455 BY SIMILARITY.
FT DISULFID 1462 1473 BY SIMILARITY.
FT DISULFID 1482 1497 BY SIMILARITY.
FT DISULFID 1484 1497 BY SIMILARITY.
FT DISULFID 1616 1627 BY SIMILARITY.
FT DISULFID 1622 1636 BY SIMILARITY.
FT DISULFID 1638 1651 BY SIMILARITY.
FT DISULFID 1657 1672 BY SIMILARITY.
FT DISULFID 1667 1681 BY SIMILARITY.
FT DISULFID 1683 1696 BY SIMILARITY.
FT CARBOHYD 339 339 POTENTIAL.
FT CARBOHYD 370 370 POTENTIAL.
FT CARBOHYD 416 416 POTENTIAL.
FT CARBOHYD 612 612 POTENTIAL.
FT CARBOHYD 1042 1042 POTENTIAL.
FT CARBOHYD 1242 1242 POTENTIAL.
FT CARBOHYD 1357 1357 POTENTIAL.
SQ SEQUENCE 1712 AA; 186598 MW; 70924DB1 CRC32;

Query Match 3.0%; Score 103; DB 1; Length 1712;
Best Local Similarity 34.9%; Pred. No. 9, 87e-03;
Matches 15; Conservative 12; Mismatches 12; Indels 4; Gaps 4;

DB 1032 DECLOP-RVCT-NGSCTNLESGYMSCKHKGVSPT-P-DHRHQ 1070
OY 159 NHCLDAKACNLNDCKKLRSSYISICNREISPTERCNRKCH 201

RESULT 10
ID NOV MOUSE STANDARD: PRT: 354 AA.
AC 064299;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

DE NOV PROTEIN HOMOLOG PRECURSOR (NOVH).
 GN NOV.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-129/SV, AND ICR: TISSUE-BRAIN;
 RA SNAITH M.R., NATARAJAN D., TAYLOR L.B., CHOI C.P., MARTINERIE C.,
 RA PERBAL B., SCHOFIELD P.N., BOULTER C.A.;
 RL SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6;
 RX MEDLINE: 96204003.
 RA MARTINERIE C., CHEVALIER G., RAUSCHER F.J. III, PERBAL B.;
 RL ONCOGENE 12:1479-1492(1996).
 CC -1- FUNCTION: IMMEDIATE-EARLY PROTEIN LIKELY TO PLAY A ROLE IN CELL
 CC GROWTH REGULATION (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
 CC PROTEIN FAMILY. CEF-10/CYR61/CTCF/ELIS-12/NOV PROTEIN SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 WFEC DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).
 DR EMBL: X97863; E181580; -;
 DR EMBL: Y09257; E281106; -;
 DR EMBL: X96585; E28599; -;
 DR MGD: MGI:109185; NOV.
 DR PROSITE: PS00222; IGF_BINDING; 1.
 DR PROSITE: PS01185; CTCK_1; 1.
 DR PROSITE: PS01205; CTCK_2; 1.
 DR PROSITE: PS01208; WFEC; 1.
 KM PHOTO-ONCOGENE: GROWTH FACTOR BINDING; SIGNAL.
 FT SIGNAL. 1 21 POTENTIAL.
 FT CHAIN. 22 354 NOV PROTEIN HOMOLOG.
 FT DOMAIN. 102 168 WFEC.
 FT DISULFID. 261 298 CTCK.
 FT DISULFID. 278 312 BY SIMILARITY.
 FT DISULFID. 289 328 BY SIMILARITY.
 FT DISULFID. 292 330 BY SIMILARITY.
 FT DISULFID. 297 334 BY SIMILARITY.
 FT CARBOHYD. 91 91 POTENTIAL.
 FT CARBOHYD. 277 277 POTENTIAL.
 SQ SEQUENCE 354 AA; 38928 MW; 65AAEF0E CRC32;
 Query Match 2.9%; Score 97; DB 1; Length 354;
 Best Local Similarity 36.2%; Pred. No. 9.98e-02;
 Matches 17; Conservative 10; Mismatches 17; Indels 3; Caps 3;
 Db 260 KCLRTKSLKAIHLOFENGCSLYTKRFGVCSGSGRCCTPHNKT1 306
 Oy 194 RCNR-RKCHKALROFDFPVESEYTRMLFCS-COD-OACAEERRRQTI 237
 RESULT 11
 ID RL19.MYCTU STANDARD; PRT; 113 AA.
 AC Q10792;
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE 50S RIBOSOMAL PROTEIN L19.
 GN RPLS OR MTCY274.35C.
 OS MYCOBACTERIUM TUBERCULOSIS.
 OC PROKARYOTA; FIRMITICUTES; ACTINOMYCETALES; MYCOBACTERIACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RA CONNOR R., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
 RL SUBMITTED (JUN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- FUNCTION: THIS PROTEIN IS LOCATED AT THE 30S-50S RIBOSOMAL SUBUNIT
 CC INTERFACE AND MAY PLAY A ROLE IN THE STRUCTURE AND FUNCTION OF THE
 CC AMINOACYL-TRNA BINDING SITE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE L19P FAMILY OF RIBOSOMAL PROTEINS.

DR EMBL: Z74024; E248891; -;
 DR PROSITE: PS01015; RIBOSOMAL_L19; 1.
 OS RIBOSOMAL PROTEIN
 SQ SEQUENCE 113 AA; 13013 MW; 913A7AFE CRC32;
 Query Match 2.8%; Score 95; DB 1; Length 113;
 Best Local Similarity 46.2%; Pred. No. 2.10e-01;
 Matches 12; Conservative 4; Mismatches 10; Indels 0; Caps 0;
 Db 5 DEVDKPSLDLDIPAEVPGDTIVHYK 30
 Oy 341 DEFDNPLRNAIQAFGNGTVNVSPK 366
 RESULT 12
 ID B3AR.HUMAN STANDARD; PRT; 408 AA.
 AC P13945;
 DT 01-JAN-1990 (REL. 13, CREATED)
 DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE BETA-3 ADRENERGIC RECEPTOR.
 GN ADRB3 OR ADRB3R OR B3AR.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 89368947.
 RX EMORINE L.J., MARILLO S., BRIEND-SUTREN M.-M., PATEY G., TATE K.,
 RA DELAVIER-KLUTCHKO C., STROSBERG A.D.;
 RL SCIENCE 245:1118-1121(1989).
 RN [2]
 RP REVISIONS, SEQUENCE FROM N.A.
 RX MEDLINE: 93279311.
 RX VAN SPRONSEN A., NAHMIAS C., KRIEF S., BRIEND-SUTREN M.-M.,
 RA STROSBERG A.D., EMORINE L.J.;
 RL EUR. J. BIOCHEM. 213:1117-1124(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 93285320.
 RA LELIAS J.M., KAGHAD M., RODRIGUEZ M., CHALON P., BONNIN J.,
 RA DUPRE I., DELPECH B., BENSARD M., LEFUR G., FERRARA P., CAPUT D.,
 RL FEBS LETT. 324:127-130(1993).
 RN [4]
 RP SEQUENCE OF 392-408 FROM N.A.
 RX MEDLINE: 93125503.
 RA GRANNEMAN J.G., LAHNER K.N., RAO D.D.;
 RL MOL. PHARMACOL. 42:964-970(1992).
 RN [5]
 RP VARIANT ARG-64.
 RA CLEMENT K., VAISSE C., MANNING B.S.J., BASDEVANT A., GUY-GRANDI N.,
 RA RUIZ J., SILVER K.D., SHULDINER A.R., FROGUEL P., STROSBERG A.L.;
 RL NEW ENGL. J. MED. 333:352-354(1995).
 RN [6]
 RP VARIANT ARG-64.
 RX MEDLINE: 96361936.
 RA FUJISAWA T., IREGAMI H., YAMATO E., TAKEKAWA K., NAKAGAWA Y.,
 RA HAMADA Y., OGA T., UEDA H., SHINTANI M., FUKUDA M., OGIHARA I.;
 RL DIABETOLOGIA 39:349-352(1996).
 RN [7]
 RP VARIANT ARG-64.
 RX MEDLINE: 96217306.
 RA CANDELORE M.R., DENG L., TOTA L.M., KELLY L.J., CASCIERI M.A.,
 RA STRADER C.D.;
 RL ENDOCRINOLOGY 137:2638-2641(1996).
 CC -1- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-
 CC INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G-
 CC PROTEINS. BETA-3 IS INVOLVED IN THE REGULATION OF LIPOLYSIS AND
 CC THERMOGENESIS.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: MAINLY IN ADIPOSE TISSUES.
 CC -1- POLYMORPHISM: THE VARIANT ARG-64 SEEMS TO BE ASSOCIATED WITH
 CC WEIGHT GAIN (OBESITY) AND TO IS ALSO ASSOCIATED WITH

CC SUSCEPTIBILITY TO NON-INSULIN-DEPENDENT DIABETES MELLITUS (NIDDM).
 CC -1 SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: M29932; G178896; ALT_TERM.
 DR EMBL: X70812; E67465; ALT_SEQ.
 DR EMBL: X72861; G328095; -
 DR EMBL: X70811; G312397; -
 DR EMBL: X70812; E281052; ALT_SEQ.
 DR EMBL: X70812; E280975; ALT_SEQ.
 DR EMBL: S53291; G263089; -
 DR PIR: A41348; A41348.
 DR PIR: S33751; S33751.
 DR GCRDB: GCR_0051; -
 DR GCRDB: GCR_0547; -
 DR GCRDB: GCR_0595; -
 DR GCRDB: GCR_0735; -
 DR MIM: 109691; -
 DR PROSITE: PS00237; G-PROTEIN_RECEPTOR_1.
 KM G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
 KM MULTIGENE FAMILY; PHOSPHORYLATION; LIPOPROTEIN; PALMITATE;
 KM POLYMORPHISM; DIABETES; OBESITY.
 FT DOMAIN 1 36
 FT TRANSMEM 37 62
 FT DOMAIN 64 72
 FT TRANSMEM 73 91
 FT DOMAIN 92 111
 FT TRANSMEM 112 133
 FT DOMAIN 134 155
 FT TRANSMEM 156 178
 FT DOMAIN 179 203
 FT TRANSMEM 204 225
 FT DOMAIN 226 292
 FT TRANSMEM 293 314
 FT DOMAIN 315 326
 FT TRANSMEM 327 347
 FT DOMAIN 348 408
 FT CARBOHYD 8 8
 FT CARBOHYD 26 26
 FT DISULFID 110 189
 FT LIPID 361 361
 FT VARIANT 64 64
 FT SEQUENCE 408 AA; 43519 MW; 47AEC098 CRC32;
 Query Match 2.88; Score 95; DB 1; Length 408;
 Best Local Similarity 39.4%; Pred. No. 2.10e-01;
 Matches 13; Conservative 10; Mismatches 8; Indels 2; Gaps 2;
 Db 296 LMGFTLCMLPEFLANVRAIGSPSLVGPAPF 328
 Qy 1 MILAN-VFC-LFFFLDDTLRLSPSLGPEL 31
 RESULT 13
 ID CYS2_HAECO STANDARD: PRT: 342 AA.
 AC P25733:
 DT 01-MAY-1992 (REL. 22, CREATED)
 DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE CATHEPSIN B-LIKE CYSTEINE PROTEINASE 2 PRECURSOR (EC 3.4.22.-).
 GN AC-2.
 OS HAEMONCHUS CONTORTUS.
 OC EUKARYOTA; METAZOA; ACCELOMATES; NEMATODA; SECERNENTEA; SPIRURIDA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 91218800.
 RA PRATT D., COX G.N., MILHAUSEN M.J., BOISVENUE R.J.:
 RL MOL. BIOCHEM. PARASITOL. 43:181-192(1990).
 CC -1 FUNCTION: EXPRESSION OF THE PROTEASE CORRELATES WITH BLOOD-FEEDING
 CC AND SUGGESTS A ROLE FOR THE PROTEASE IN BLOOD DIGESTION.
 CC -1 DEVELOPMENTAL STAGE: AT LOW LEVEL IN THE THIRD AND FOURTH-STAGE
 CC LARVAE, AND ABUNDANT IN ADULT WORMS.
 CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1; ALSO KNOWN AS THE
 CC PAPAIN FAMILY OF THIOL PROTEASES.
 CC -1 SIMILARITY: STRONGEST, TO CATHEPSIN B.

DR EMBL: M60213; G159165; -
 DR EMBL: M60212; G159165; JOINED.
 DR PIR: A44965; A44965.
 DR HSSP: P07858; IHUC.
 DR PROSITE: PS00139; THIOL_PROTEASE_CYS_1.
 DR PROSITE: PS00639; THIOL_PROTEASE_HIS_1.
 DR PROSITE: PS00640; THIOL_PROTEASE_ASN_1.
 KM HYDROLASE; THIOL PROTEASE; ZYMOGEN; GLYCOPROTEIN; SIGNAL;
 KM MULTIGENE FAMILY.
 FT SIGNAL 1 7
 FT PROPEP 86 86
 FT CHAIN 87 342
 FT ACT_SITE 114 114
 FT ACT_SITE 114 114
 FT ACT_SITE 285 285
 FT ACT_SITE 305 305
 FT DISULFID 100 128
 FT DISULFID 111 156
 FT DISULFID 147 214
 FT DISULFID 148 152
 FT DISULFID 185 218
 FT DISULFID 193 205
 FT CARBOHYD 99 99
 FT CARBOHYD 138 138
 FT CARBOHYD 198 198
 FT SEQUENCE 342 AA; 38406 MW; 89092341 CRC32;
 Query Match 2.7%; Score 91; DB 1; Length 342;
 Best Local Similarity 33.3%; Pred. No. 8.96e-01;
 Matches 12; Conservative 9; Mismatches 12; Indels 3; Gaps 3;
 Db 200 TYGEC-RGTAPTPPC-RRKCRPGVKMY-RIDKRY 232
 Qy 180 SYISICNREISPTERCNRKCHKALROFEDVPSSEY 215
 RESULT 14
 ID CYS1_HAECO STANDARD: PRT: 342 AA.
 AC P19092:
 DT 01-NOV-1990 (REL. 16, CREATED)
 DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE CATHEPSIN B-LIKE CYSTEINE PROTEINASE 1 PRECURSOR (EC 3.4.22.-).
 GN AC-1.
 OS HAEMONCHUS CONTORTUS.
 OC EUKARYOTA; METAZOA; ACCELOMATES; NEMATODA; SECERNENTEA; SPIRURIDA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-ISOLATE BPL1;
 RX MEDLINE: 90348715.
 RA COX G.N., PRATT D., HAGEMAN R., BOISVENUE R.J.:
 RL MOL. BIOCHEM. PARASITOL. 41:25-34(1990).
 CC -1 FUNCTION: EXPRESSION OF THE PROTEASE CORRELATES WITH BLOOD-FEEDING
 CC AND SUGGESTS A ROLE FOR THE PROTEASE IN BLOOD DIGESTION.
 CC -1 DEVELOPMENTAL STAGE: AT LOW LEVEL IN THE THIRD AND FOURTH-STAGE
 CC LARVAE, AND ABUNDANT IN ADULT WORMS.
 CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1; ALSO KNOWN AS THE
 CC PAPAIN FAMILY OF THIOL PROTEASES.
 CC -1 SIMILARITY: STRONGEST, TO CATHEPSIN B.
 DR EMBL: M31112; G159173; -
 DR PIR: A45524; A45524.
 DR HSSP: P07858; IHUC.
 DR PROSITE: PS00139; THIOL_PROTEASE_CYS_1.
 DR PROSITE: PS00639; THIOL_PROTEASE_HIS_1.
 DR PROSITE: PS00640; THIOL_PROTEASE_ASN_1.
 KM HYDROLASE; THIOL PROTEASE; ZYMOGEN; GLYCOPROTEIN; SIGNAL;
 KM MULTIGENE FAMILY.
 FT SIGNAL 1 7
 FT PROPEP 86 86
 FT CHAIN 87 342
 FT ACT_SITE 114 114
 FT ACT_SITE 285 285
 FT ACT_SITE 305 305
 FT SEQUENCE 342 AA; 38406 MW; 89092341 CRC32;
 Query Match 2.7%; Score 91; DB 1; Length 342;
 Best Local Similarity 33.3%; Pred. No. 8.96e-01;
 Matches 12; Conservative 9; Mismatches 12; Indels 3; Gaps 3;

FT DISULFID 100 128 BY SIMILARITY.
 FT DISULFID 111 156 BY SIMILARITY.
 FT DISULFID 147 214 BY SIMILARITY.
 FT DISULFID 148 152 BY SIMILARITY.
 FT DISULFID 185 218 BY SIMILARITY.
 FT DISULFID 193 205 BY SIMILARITY.
 FT DISULFID 99 99 POTENTIAL.
 FT CARBOHYD 138 138 POTENTIAL.
 FT CARBOHYD 198 198 POTENTIAL.
 FT CARBOHYD 296 296 POTENTIAL.
 SQ SEQUENCE 342 AA; 38459 MW; 280E7705 CRC32;

Query Match 2.7%; Score 91; DB 1; Length 342;
 Best Local Similarity 32.3%; Pred. No. 8.96e-01;
 Matches 12; Conservative 9; Mismatches 12; Indels 3; Gaps 3;

Db 200 TYGEC-RGTAPTPC-KKCRPGVKKMY-RIDKRY 232
 QY 180 SYISCNREISPTERCNRKCKALKALROFDRVPSEY 215

RESULT 15
 ID ASP2_BLAG STANDARD; PRT: 352 AA.
 AC P54958;
 DT 01-OCT-1996 (REL. 34, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE ASPARTIC PROTEASE BLA G 2 PRECURSOR (EC 3.4.23.-) (ALLERGEN BLA G II).
 OS BLATTELLA GERMANICA (GERMAN COCKROACH).
 OC EUKARYOTA; METAZOA; ARTHROPODA; INSECTA; BLATTODEA.
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE: 95370299.
 RA ARRUDA L.K., VAILES L.D., MANN B.J., SHANNON J., FOX J.W.,
 RA VEDVICK T.S., HAYDEN M.L., CHAPMAN M.D.;
 RL J. BIOL. CHEM. 270:19563-19568(1995).
 CC -1- FUNCTION: MAJOR ALLERGEN; FUNCTIONS AS A DIGESTIVE ENZYME IN THE
 CC COCKROACH.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1; ALSO KNOWN AS THE
 CC EUKARYOTIC ASPARTYL PROTEASES FAMILY.
 DR EMBL: U28863; G1176397; -.
 DR PROSITE: PS00141; ASP_PROTEASE; FALSE_NEG.
 KW HYDROLASE; ASPARTYL PROTEASE; SIGNAL; ALLERGEN; ZMOGEN.
 FT SIGNAL 1 ?
 FT PROPEP 1 ?
 FT CHAIN 25 24 REMOVED IN MATURE FORM.
 FT ACT_SITE 35 35 ASPARTIC PROTEASE BLA G 2.
 FT ACT_SITE 239 239 BY SIMILARITY.
 FT CARBOHYD 117 117 POTENTIAL.
 FT CARBOHYD 295 295 POTENTIAL.
 FT CARBOHYD 340 340 POTENTIAL.
 SQ SEQUENCE 352 AA; 38558 MW; 23F3B608 CRC32;

Query Match 2.7%; Score 91; DB 1; Length 352;
 Best Local Similarity 32.3%; Pred. No. 8.96e-01;
 Matches 20; Conservative 16; Mismatches 20; Indels 6; Gaps 6;

Db 34 FINTOYAGITKIGNONF-LT-VFDSISGN-VVVA-SQECVGACVCPNL-OKYEKLPKY 88
 QY 123 YEASPYEPVTSRLSDIFRLASIFSGTGADPYVASKSNHCLDAKAC-NLNDNCKKLRSY 181
 Db 89 IS 90
 QY 182 IS 183

Search completed: Mon Mar 8 14:06:44 1999
 Job time : 51 secs.

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 M E S S A G E
 (TM)

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MPsrch.jp protein - protein database search, using Smith-Waterman algorithm
 Run on: Mon Mar 8 14:53:57 1999; Maspar time 17.15 Seconds
 779.553 Million cell updates/sec
 Tabular output not generated.

Title: >US-08-866-354-43
 Description: (1-498) from US08866354.pep
 Perfect Score: 2337
 Sequence: 1 MVXXLXXXXPPXXXXMLXL.....XLPVLMFLALXLSXXXX 498

Scoring table: PAM 150
 Gap 11

Searched: 74019 seqs, 26840295 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: swiss-prot36
 1:swissprot

Statistics: Mean 45.078; Variance 68.218; scale 0.661

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1803	77.2	468	1	GNDR_RAT	0.00e+00
2	1788	76.5	464	1	GNDR_HUMAN	0.00e+00
3	1777	76.0	463	1	NTRR_MOUSE	0.00e+00
4	1772	75.8	468	1	GNDR_MOUSE	0.00e+00
5	1758	75.2	464	1	GNDR_HUMAN	0.00e+00
6	1599	68.4	469	1	GNDR_CHICK	0.00e+00
7	1561	66.8	465	1	NTRR_CHICK	0.00e+00
8	108	4.6	2524	1	NOTC_XENLA	6.55e-04
9	105	4.5	2871	1	FBN1_MOUSE	3.15e-03
10	104	4.5	2871	1	FBN1_HUMAN	2.18e-03
11	102	4.4	381	1	DHB2_MOUSE	6.92e-03
12	102	4.4	2871	1	FBN1_BOVIN	6.92e-03
13	97	4.2	1964	1	NTRC4_MOUSE	4.59e-02
14	97	4.2	3051	1	YBHC_MOUSE	4.59e-02
15	95	4.1	427	1	YBHC_ECOLI	9.60e-02
16	95	4.1	816	1	NEL_MOUSE	1.98e-01
17	93	4.0	498	1	YMS5_MOUSE	1.98e-01
18	93	4.0	816	1	NEL_RAT	1.98e-01
19	94	4.0	879	1	LDLR_RAT	1.38e-01
20	93	4.0	1480	1	SLIT_DRONE	1.98e-01
21	93	4.0	2444	1	NTRC1_HUMAN	1.98e-01
22	90	3.9	382	1	ALBU_RANCA	5.76e-01
23	92	3.9	383	1	DLK_HUMAN	2.84e-01

RESULT ID	1	STANDARD	PRT	468 AA.	ALIGNMENTS
AC	GNDR_RAT				
AC	062997				
DT	01-NOV-1997 (REL. 35, CREATED)				
DT	01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)				
DT	15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)				
DE	GNDR RECEPTOR ALPHA PRECURSOR (GNDR-ALPHA) (TGF-BETA RELATED				
DE	NEUROTROPHIC FACTOR RECEPTOR 1) (RET LIGAND 1).				
GN	GFRA1 OR GDNFR OR TRNRI OR RETLI.				
OS	RATTUS NORVEGICUS (RAT).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EUTHERIA; RODENTIA.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-WISTAR; TISSUE-KIDNEY;				
RA	MEDLINE: 97322356				
RA	SANTOLA M., HESSON C.A., WORLEY D.S., CARMILLO P., EHRENFELDS C.,				
RA	WALUS L., ROBINSON S., JAWORSKI G., WEI H., TITARD R., WHITTY A.,				
RA	PEPINSKY R.B., CAPE R.L.;				
RA	PROC. NATL. ACAD. SCI. U.S.A. 94:6238-6243(1997).				
RA	FOX G.M., HU Z., CUPPLES R., LOUIS J.-C., HU S., ALTHROCK B.W.,				
RA	CELL 85:1113-1124(1996).				
RL	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-WISTAR; TISSUE-KIDNEY;				
RA	MEDLINE: 96273032				
RA	TREANOR J.J.S., GOOGAN L., DE SAUVAGE F., STONE D.M., POULSEN K.T.,				
RA	BECK C.D., GRAY C., ARMANINI M.P., POLLOCK R.A., HEFTI F.,				
RA	PHILIPS H.S., GODDARD A., MOORE M.W., BUT-SELLO A., DAVIES A.M.,				
RA	ASAI N., TAKAHASHI M., VANDEN R., HENDERSON C.E., ROSENTHAL A.,				
RA	NATURE 382:80-83(1996).				
CC	- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED				
CC	AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR.				
CC	- SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE THOUGHT TO FORM A COMPLEX				
CC	WITH THE DISULFIDE-LINKED GDNF DIMER AND WITH 2 MOLECULES OF RET.				
CC	- TISSUE SPECIFICITY: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.				
CC	- TISSUE SPECIFICITY: EXPRESSED IN LIVER, BRAIN AND KIDNEY.				
CC	- SIMILARITY: BELONGS TO THE GDNFR FAMILY.				
DR	EMBL: U59486; G1399863; -				
DR	EMBL: U97142; G2282022; -				
KW	RECEPTOR; GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL.				
FT	SIGNAL 1 24				

FT	CHAIN	25	430	GNF RECEPTOR ALPHA.
FT	PROPEP	431	460	HYDROPHOBIC. REMOVED DURING MATURATION (POTENTIAL).
FT	DOMAIN	362	369	POLY-THR.
FT	CARBOHYD	59	59	POTENTIAL.
FT	CARBOHYD	347	347	POTENTIAL.
FT	CARBOHYD	406	406	POTENTIAL.
FT	LIPID	430	430	GPI-ANCHOR (POTENTIAL).
FT	SEQUENCE	468 AA:	51649 MW:	6A7A2B2A CRC32:

Query Match	77.28;	Score 1803;	DB 1;	Length 468;
Best Local Similarity	53.38;	Pred. No. 0.00e+00;		
Matches 255;	Conservative	23;	Mismatches 183;	Indels 17;
				Gaps 12;

Db 1 MELVATYALPLDLMLMAEYSGDRL-DCVKASDGLKSGSSTYRTLRQCVAKRET 58
16 MxLKLSLALPLXXXLGLAELXGXRLXXDCVAXXXXXXKAXXKXSYRTLRLROCMAXXXX 75
Qy 59 NPSITSGLEAFRDE--CPSAMAIKQSLVYNPECFEGKKEPKENRTLTAWSNVQSG--CNTI 118

Db 116 LEDSYEE-VNSRLSDIFRAVPTISDVFOQVEYEHISKGNCCDAAKACNLDCTCKKYSAY 174

QY 136 LEXSPEYEVYTSRLSDIPRXSXXXXXXXXXXXXXXXXXXCLDAKACNLNDXCCKLSAY 195

Db 175 ITPCTISMSN-EVCNRRKCHALQOFDPKPAKHSYGLMFCSCR--DIACCTERRQTIIP 231

D
y

196 IXCAXXXXXXERCNRRCRHALNQFDPKVPYXXHXHYGLFLFCSCXXXDXACERRRQITXP 255

232 VCSEIERERPNCLSDCKTNYICRSRLADFTINCQPESHSSVSNCLKENAYDCLLAYSG 293

Db 292 LIGTVMPTNYVDS - SIS - VAPMCDCSNGSDIEDCLFLNFKDNTCLKNAIOAFNGS 349
 ||||| : |||| | || | : || || |
Oy 316 LIGTAMPNIYDSKTXAXAPMCCKRSGGXAECEERELFLFXANPCLKNALIOAFNGX 375/5

Db		350	DVTMMQPA - P - PVQTATTATTTAFRVKNKP - LGSAGSENE - IPTHTLPDPCANLQOKL 403
	: :		
Oy		376	XXXXXXXXXXPFESVXXXXXTXTYAXARXXXPSLXXXXSKXXXXXTYVXXXXCXIXLOXKL 435

[illegible]

RESULT 2
D NTRR_HUMAN STANDARD; PRT; 464 AA.
AC 000451;
DT 01-NOV-1997 (REL. 35, CREATED)

D1 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE NEURITRIN RECEPTOR ALPHA PRECURSOR (NTRN-ALPHA) (NRTNR-ALPHA) (TGF-BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 2) (GNFR RECEPTOR BETA) (GNFR-BETA).
DE

GN GFFA2 OR GDNFRB OR TRNR2.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAEOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.

RN
 RN
 (2)
 SEQUENCE FROM N.A.
 RP
 RX
 MEDLINE: 97325791.
 BALOH R.H., TANSEY M.G., GOLDEN J.P., CREEDON D.J.,
 RA
 HEUCKEROFF R.O., KECK C.L., ZIMONJIC D.B., POPESCU N.C.,

RA JOHNSON .M. JR., MILBRANDT J. ;
RL NEURON 18:793-802(1997) .
-1- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NRTN-INDUCED
CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR. ALSO ABLE
CC TO MODULATE GDNF STIMULATING THROUGH THE RET NEUROTROPIC KINASE.

CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
CC SIMILARITY).

CC -1- ALTERNATIVE PRODUCTS: A SHORT FORM IS PRODUCED BY ALTERNATIVE
CC SPLICING IN BOTH BRAIN AND PLACENTA.
CC -1- SIMILARITY: BELONGS TO THE GGNFR FAMILY.
DR EXBL: AF002700; G2145080; -.

DR	MIM: 601956; -	
KM	RECEPTOR; GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL;	
KW	ALTERNATIVE SPLICING.	
FT	SIGNAL	21
FT	CHAIN	22
FT	CHAIN	444
FT	CHAIN	POTENTIAL. TGF-BETA RELATED NEUROTROPHIC FACTOR

FT	PROPER	445	464	RECEPTOR 2. HYDROPHOBIC. REMOVED DURING MATURATION. (POTENTIAL).
FT	CARBOHYD	52	52	POTENTIAL.
FT	CARBOHYD	357	357	POTENTIAL.
FT				

FT CARBOHYD	413	413	POTENTIAL.
FT LIPID	444		GPI-ANCHOR (POTENTIAL).
FT VARSPLIC	14	146	MISSING (IN SHORT FORM).
SO SEQUENCE	464 AA.	51558 MW;	3674BBFB CRC32.

Query Match	76.5%	Score 1788;	DB 1;	Length 464;
Best Local Similarity	56.2%	Pred. No. 0.00e+00;		
Matches 262;	Conservative	17;	Mismatches 166;	Indels 21;
			Gaps	9

[illegible]

07 EXXXXXXXXXXAEXLXMSLVDRCRKRMRKEXCLITYSHXHXLXGNXKXLEXPYEP 14

Qy 144 XTSTRSLDFRXXSXXXXXXSSNCLDAACMLNDCKRKLRSAYIXXCXXX 20

Dd 190 SPTEERNRKKAKALRPFDFRVPSTYTRMLFGCG--DQACERRRQIILLDSCTYDKE 24

0y	204	5X5ERCNR8RCKHAKLRQFEDFKVXXHHYGMFLCSCXXHDXACXERRRQIITXSCSEYXHE	26
0y	248	KPNCEDLDREVCTDHLKCSRLADPHANCRASTQYTWISPCADNYQACLG5YAGMIGFDMTP	30
0y	264	KPNCIDLRRXCTDHLKCSRLADFEJTNKXXXXRVKSCXXANXXCCLAAVXGICGTMMP	32

D_b 308 NYVDSSPTGIVVSPMCSCRGSGNNEECCENFLRDFTENPCLRNAIOAFNGTIDVANVSPKG
||||| : |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
324 NYVDSSXTXXXXXAPMPCXCRGSGKNNEECENFLAEFXFNPCPLMAIALIOAFNGXXXXXXXXX TR

```

Db      368 --PSF-----QA*QAPRVERKPTSLPDDLSDSPSTLGTSVITTCFSVGEGLKANNSKL. 1
          |         :   |   |   |   |   |   |   |   |   |   |   |   |   |
OY     384 XNPFSEVXXXXXTTAKARVXXXXPSSLXXXXSSXXXXLTATVXXXCXYLQXOLKNANSHNA. 4

```

Db 419 SMCETELTNIIIGSNKVIKRNPSGRARPSAALTIVSLVPMKQAL 464
 || ||||| | : | |||| |
 QY 444 XKCFEELTTNNXXSXGXXXXXXIXXXSXAXAPSKALXLPVLMPT -AL 488

RESULT	3	
ID	NTR_MOUSE	STANDARD; PRT; 463 AA.
AC	008842;	
DT	01-NOV-1997 (REL. 35, CREATED)	

DE (GDNF-RECEPTOR RETA)
DE BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 2) (GDNF RECEPTOR RETA)
DE NEURTURIN RECEPTOR ALPHA PRECURSOR (NTRN-ALPHA) (NNTN-ALPHA) (Tg:)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE (GDNF-RECEPTOR RETA)

GN GFERA2 OR GDNFEB OR TRNFR2.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUTHERIA: RODENTIA.

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97325791.
 ZA BALOH R.H., TANSEY M.G., GOLDEN J.P., CREEDON D.J.,

DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF- β RELATED
DE NEUROTROPHIC FACTOR RECEPTOR 1).
OS GFAL OR GDNFR OR TRNRI.
OS MOS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA:
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=DORSAL ROOT GANGLION;
RA MATABE K.;
RL SUBMITTED (FEB-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED
CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR (BY
CC SIMILARITY).
CC -1- SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE THOUGHT TO FORM A COMPLEX
CC WITH THE DISULFIDE-LINKED GDNF DIMER AND WITH 2 MOLECULES OF RET
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
CC SIMILARITY). BELONGS TO THE GDNFR FAMILY.
CC -1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.
DR EMBL; AB000800; G1816442; -.
KM RECDP; MG1:1100842; GFAL.
KW RECEPTOR; GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 430
FT PROPEP 431 468
FT DOMAIN 362 369
FT CARBOHYD 59 59
FT CARBOHYD 347 347
FT CARBOHYD 406 406
FT LIPID 430 430
SQ SEQUENCE 468 AA; 51782 MW; 6C64C182 CRC32;
Query Match 75.8%; Score 1772; DB 1; Length 468;
Best Local Similarity 51.9%; Pred. No. 0.00e+00;
Matches 248; Conservative 29; Mismatches 184; Indels 17; Gaps 12.

ID	GDNFR_HUMAN	STANDARD:	PRT:	464 AA.
AD	P56159:			
DT	01-NOV-1997 (REL. 35, CREATED)			
DT	01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)			
DT	15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)			
DE	GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF-BETA RELATED			
DE	NEUROTROPHIC FACTOR RECEPTOR 1).			
GN	GPR41 OR GDNFR4 OR TRNR1.			
OC	HOMO SAPIENS (HUMAN).			
OC	EUDAROTA: METAFOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:			
OC	EUTHERIA: PRIMATES.			
RA	[1]			
RA	SEQUENCE FROM N.A.			
RA	TISSUE-SUBSTANTIA NIGRA;			
RA	MEDLINE; 96270513.			
RA	JING S., MEN D., YU Y., HOLST P.L., LUO Y., FANG M., TAMIR R.,			
RA	ANTONIO L., HU Z., CUPPLES R., LOUIS J.-C., HU S., ALTHROCK B.W.,			
RA	FOX G.M., HU Z., CUPPLES R., LOUIS J.-C., HU S., ALTHROCK B.W.,			
RA	CELL 85:1113-1124(1996).			
CC	-1- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED			
CC	AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR (BY			
CC	SIMILARITY).			
CC	-1- SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE THOUGHT TO FORM A COMPLEX			
CC	WITH THE DISULFIDE-LINKED GDNF DIMER AND 2 MOLECULES OF RET (BY			
CC	SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY			
CC	SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.			
DR	MM; 601496; -.			
FM	RECEPTOR: GLYCOPROTEIN: GPI-ANCHOR; MEMBRANE; SIGNAL.			
FT	SIGNAL	1	24	POTENTIAL.
FT	CHAIN	25	428	GDNF RECEPTOR ALPHA.
FT	PROPEP	429	464	HYDROPHOBIC, REMOVED DURING MATURATION
FT				(POTENTIAL).
FT	DOMAIN	361	368	POLY-THR.
FT	CARBOHYD	59	59	POTENTIAL.
FT	CARBOHYD	346	346	POTENTIAL.
FT	CARBOHYD	405	405	POTENTIAL.
FT	LIPID	428	428	GPI-ANCHOR (POTENTIAL).
FT	SEQUENCE	464 AA:	51291 MM;	2C8C3574 CRC32;

Query Match	75.2%	Score	1758:	DB 1:	Length	464:			
Best Local Similarity	75.6%	Pred.	No. 0.0ae+00:						
Matches	254:	Conservative	24:	Mismatches	186:	Indels	19:	Gaps	14:
Db	1	MFLATLYFALPLDLLLSAEVSGGDLT--DCVKASDQCLKEBQSCSTRYRTLROCVAKRET	58						
16	MXLKLSLSLATPLRLLXLLGGAELXGXRLXDCVAXXKXCAEXKSCXXYRTLROCXAGXX	75							
Db	59	NFSLASGLAEAD--CRSAMALNOKSLYRNCRCRGMKKENCLRIYWSMQSQ--GNDL	115						
QY	76	NTXIASGEXXXXXXXKXAMEXLXSSLYIDRCRGMKKEXXCXITWShXXLXKXNXX	135						
Db	116	LEDSPEYED--VNSRLSDIFRRVVPFISDVEQVEHPIPKGNNCIDAAKACNLDDICKKRYAS	174						
QY	136	LEKSPYEPXYVTSRLSDIFRXXSXXXXXXDXKXKSNXCIDAAKACNLNDXCKKLASAY	195						
Db	175	ITPCTTSYVN--DVNCRKCHKALQOFDDKYPAKASTGYMLFQSCS--DIACERRRQTIYP	231						
QY	196	IXKXXXXXXKXERCNRRRCHRALQOFDDKYPXHXGYMLFQSCXXXXXACXERRRQTIYP	255						
Db	232	VCSYEERKPNCL--LQDSCKTNYICRSLRDLDFPNCQPESSVSGLCKENYADCLLAYSG	290						
QY	256	SCSEIXXEXKPRCDDLKXKCRIDKLCRSLRDLDFXNCCXXXXXXKXVASCAXHXXCLXAYXG	315						
Db	291	LIGVTMPNYIDSS--SLK--VAPWDCGNSGNDLEBCLFLNFQKNTCLKNALQAFNGS	348						
QY	316	LIGVTMPNYVDSSXSTXXVAPWMCXCGSGNGXKXEECEKFLAEFXFNPCLNALQAFNGX	375						
Db	349	DVTWQQA--P--PVQTTTATTTALRVKNKP--LGPAGSENE--IPHYVLPCCANLQAKL	402						
QY	376	XXXXXXXXXXPFSEVXXXXXXXTYIAKXVXXXXPSLXXXXXXKXKXLTXYVXXXXCXKLAQXL	435						

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Db      403 KSVSGNTHLCSN-GNEKEKELGASSHTTMSAPSCGLSPLYVVAALSTLSLT 461
Qy      436 KKNSSXEXXXCPXELTTNXXXXXXXGXKKXIXXXSXAXPSKXLXLPVLMTALAYLSXX 495
Db      462 ETS 464
Qy      496 XXS 498

RESULT        6
ID    GDNF_CHICK STANDARD; PRT; 469 AA.
AC    013156;
DT     01-NOV-1997 (REL. 35, LAST SEQUENCE)
DT     01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT     15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE     GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF-BETA RELATED
GN     NEUROTROPHIC FACTOR RECEPTOR 1).
OS     GALUS GALLUS (CHICKEN).
OC     EURAROTIA, METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHA;
NC     GALLIFORMES.
RN     (1)
RP     SEQUENCE FROM N.A.
RC     TISSUE=RAIN:
RA     BUI-BELLO A., ADU J., PINON L.G.P., HORTON A., THOMPSON J.,
RL     ROSENTHAL A., CHINCHETRU M., BUCHMAN V.L., DAVIES A.M.;
RL     NATURE 387:721-724(1997).
CC     -1- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED
CC     AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR (BY
CC     SIMILARITY).
CC     -1- SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE THOUGHT TO FORM A COMPLEX
CC     WITH THE DISULFIDE-LINKED GDNF DIMER AND WITH 2 MOLECULES OF RPI
CC     (BY SIMILARITY).
CC     -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (1)
CC     (SIMILARITY).
CC     -1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.
DR     EMBL: U90541: G2131803; -
KM     RECEPTOR: GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL.
FT     SIGNAL          1       27
FT     CHAIN           28      430
FT     PROPEP          431      469
FT     DOMAIN          361      368
FT     CARBOHYD         62       62
FT     CARBOHYD        163      163
FT     CARBOHYD        346      346
FT     CARBOHYD        405      405
FT     LIPID           430      430
SO     SEQUENCE 469 AA; 52043 MW; C8D241C9 CRC32;.

Query Match      68.4%; Score 1599; DB 1; Length 469;
Best Local Similarity 49.3%; Pred. No. 0.00e+00;
Matches 237; Conservative 31; Mismatches 189; Indels 24; Gaps 17

Db      1 MFALLIYALDLADLVILSAEVSGLPGGDRLDVCYAASQCLEKGSCSTRIRPLRQCVAGKE 60
Qy      16 MXLLSLIALDLPLXXXHLGGAELDGXXXRLXX-DCVAXAXXXCAEXXCXYRFLRQCGAGXX 74
Db      61 SNFSRATGLEAKDE--CKSAMEALKOKSLNYLCRCRGKMGKEKNCLTRIYMSYQSLO-GND 117
Qy      75 XNTYLASGXEXXXXXXXCXAAEXLXSSSLDCCRKRGMKEKEXKLXIYWSHXHXLXGXNX 134
Db      118 LLEDSPYP-VNSRLSDIFRLAPIVSY--EPVLS-KGNCLDAAKACNLDTCKRFPSA 172
Qy      135 XLESPPPYXTSRSLDFIRXSXXSXXXXXXSNXNNCLDAAKACNLNDXCKKLRSA 194
Db      173 YITCTGSTSN-EICNKRKCHKALRLFEDKVPFHSHSGMFCGR--DVACTERRQTV 229
Qy      195 YIXXCMXXSXEXECNRKCHKALRQFFEDKVPXHXXGMFCSCXXXDXDACXERRQTV 254
Db      230 PVCSGEVEREKNCNLDESCKKNYICGSRLADFNTNQPSRSYSGCLKENVADCLLAY 289
Qy      255 PCSGYEXEKERPNDLXXXCRTDLCNSRLADFTTNCCCCXXRXVYSXAXANYYXCLAIYX 314

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ID	NR	CHICK	STANDARD	PRT	465 AA.
DB	220	GLICVMPNPNYIDS-SLS-VAPMCDGNSGNDIDECKRFLNFQDQTCLNKNAIOAGNG	347		
OY	315	GLIGTKMTPNVDSDSIXXVAPMCXCGSGNXXEBCFKLFXFXNPNCLNNAIOAFNG	374		
DB	348	TDVNVWQ-----PIIPVQTTTATTTATTSRLKNTGS-ETTNNIEPT-HND-SFACANLOAQK	400		
OY	375	XXXXXXXXXXXXXPKPSVXXXXXTXTAKXVXXXXPSLXXXXXKXKXLLTXVXXXXKXKXLOXQ	434		
DB	401	KRKSNEVDTELCLNENAIKQNDTPGVSTSHISSENSEFALFTSYPPSTPLTMTIALSLF	460		
OY	435	L-KNXXSXKXKXKXCFELTNTNXXKXSGXXXX-IXXXSXKXKXPSKXSLXLP-VLMTLALXL	491		
DB	461	L 461			
OY	492	L 492			
RESULT	7	STANDARD	PRT	465 AA.	
ID	NR	CHICK	STANDARD	PRT	465 AA.
AC	01357				
DT	01-NOV-1997	(REL. 35, CREATED)			
DT	01-NOV-1997	(REL. 35, LAST SEQUENCE UPDATE)			
DT	15-JUL-1998	(REL. 36, LAST ANNOTATION UPDATE)			
DE	NEUTROTRIN RECEPTOR ALPHA PRECURSOR (NTRN-ALPHA) (GDNF				
DE	RECEPTOR BETA) (GDNFR-BETA).				
GN	GFR22 OR GDNFRB				
OS	GALLUS GALLUS (CHICKEN).				
OC	EUAROTIA; METAEOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;				
OC	GALLIFORMES.				
AN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-BRAIN:				
RA	BUU-BELLO A., ABU J., PINON L.G.P., HORTON A., THOMPSON J.,				
RA	ROSENTHAL A., CHINCHEIRO M., BUCHMAN V.L., DAVIES A.M.;				
RL	NAURE 387:721-724(1997).				
CC	-1- FUNCTION: RECEPTOR FOR NEUTROTRIN, MEDIATES THE NRTN-INDUCED				
CC	AUTOPIHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR. ALSO ABLE				
CC	TO MEDIANE GDNF SIGNALING THROUGH THE RET TYROSINE KINASE				
CC	RECEPTOR (BY SIMILARITY)				
CC	-1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.				
CC	-1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.				
CC	-1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.				
DR	EMPL; U90542; G213805; -				
KW	RECEPTOR; GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL.				
FT	SIGNAL	1	21		
FT	CHAIN	22	445		
FT	PROPEP	446	465		
FT	CARBOHYD	355	355		
FT	CARBOHYD	387	387		
FT	CARBOHYD	412	412		
FT	LIPID	445	445		
SO	SEQUENCE	465 AA;	51908 MW;	5CA073E4 CRC32;	
Query Match	66.8%;	Score 1561;	DB 1;	Length 465;	
Best Local Similarity	47.8%;	Pred. No. 0.00e+00;			
Matches	223;	Conservative 44;	Mismatches 177;	Indels 23;	Gaps 122;
DB	19	SLAAPSPSPGQDLOGW-RVPVDCITANKLCAAEAGSCSSRYRTLRQCLAGDRNTMLAN-K	76		
OY	24	ALPLXXLQGLGELMLKXKXLLKXDDCVAXKXKXCAEXKXCSXXYYTTLTLCQCNKXKXNTXKLSG	83		
DB	77	E-----COALEVLEQESPLVDCRCRGRMKREIOCLQVYGSIHGLAGEEFPASPEP	130		
OY	84	EXKXKXKXKXKXKXKXSLVDCRCRGRMKREKEXCLATYKXKXKXKXKXKXKXKXKXKXKXKX	143		
DB	131	ITSLSLDIFRLASIFSGM--DPATNKSNNHCLDAKACNDLNDCKRLRSGYISTGSKREI	187		
OY	144	XVTSLSLSDIFRXXSXKX	203		
DB	188	SATHECSRKCKKALROFQDNPVPSYTRYRLFLCGRK--DQCAEPRTQTYPPFSYEDKE	245		
OY	204	SXKHCRCNRKCKKALROFQDNPVPSYTRYRLFLCGRK--DQCAEPRTQTYPPFSYEDKE	263		

Db	246	KPNOLDLRNRCRADHLCRSLADLFANQCAQSOLTSCGDNVYQACLSTYTLILCFDWT	305
Qy	264	KPNOLDLRNRCRADHLCRSLADLFANQCAQSOLTSCGDNVYQACLSTYTLILCFDWT	323
Db	306	NYVDASTTSLTISWCSKSGNLEEECEFLRDPTEFNCPLRNAAIOAFNGTDMVLS	365
Qy	324	NYVDASTTSLTISWCSKSGNLEEECEFLRDPTEFNCPLRNAAIOAFNGTDMVLS	383
Db	366	PSPEITMLPVEK--SPA--L---PD-DINDSNTMY-DTSLITTTCTSIDOEGKLNKSKEQ	417
Qy	384	XXPFYSVYXXXXXTXTXKAPYXXPSLXXXXXXLLXTYVXXXXCXKLQXOLKXNXSEX	443
Db	418	SLCSEFOLTJTDMPDOKTFTVDKAKAGSRIRBARILPAPYIVLKL	464
Qy	444	XXCFE--LTTNXXXXSGXXXXXXIXXXXXXAPSLXLPVLMITAL	488
RESULT			
ID	8	STANDARD:	PRT: 2524 AA.
AC	P21783;		
DT	01-MAY-1991 (REL. 18, CREATED)		
DT	01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)		
DT	15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)		
DE	NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG PRECURSOR (NOTCH PROTEIN).		
GN	XORCH		
OS	XENOPUS LAEVIS (AFRICAN CLAWED FROG).		
OC	EUDAROTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE: 90385285.		
RA	COFFMAN C., HARRIS W., KINTNER C.;		
RL	SCIENCE 249:1438-1441(1990).		
RN	[2]		
RP	REVISIONS TO 1759-1782.		
RA	KINTNER C.;		
RL	SUBMITTED (JUN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.		
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.		
CC	-1- DEVELOPMENTAL STAGE: EXPRESSED ALMOST UNIFORMLY IN EARLY EMBRYOS.		
CC	-1- SIMILARITY: HIGH, WITH OTHER NOTCH-TYPE PROTEINS.		
CC	-1- SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.		
CC	-1- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.		
CC	-1- SIMILARITY: CONTAINS 6 ANK REPEATS.		
DR	EMBL: M33874; G1364263;		
DR	PIR: A35844; A35844.		
DR	HSSP: P20693; 1EST.		
DR	PROSITE: PS00010; ASX_HYDROXYL; 23.		
DR	PROSITE: PS00022; EGF_1; 34.		
DR	PROSITE: PS01086; EGF_2; 29.		
KW	PROSITE: PS01087; EGF_CA; 21.		
DR	DIFFERENTIATION: NEUROGENESIS; REPEAT: ANK REPEAT; EGF-LIKE DOMAIN:		
KW	TRANSMEMBRANE; SIGNAL; GLYCOPROTEIN.		
FT	SIGNAL	1	19
FT	CHAIN	20	2524
FT	DOMAIN	20	1728
FT	TRANSMEM	1729	1750
FT	DOMAIN	1751	2524
FT	DOMAIN	20	57
FT	DOMAIN	38	99
FT	DOMAIN	102	140
FT	DOMAIN	141	177
FT	DOMAIN	179	215
FT	DOMAIN	217	254
FT	DOMAIN	256	292
FT	DOMAIN	294	332
FT	DOMAIN	334	370
FT	DOMAIN	411	409
FT	DOMAIN	471	449
FT	DOMAIN	451	487
FT	DOMAIN	489	525
FT	DOMAIN	527	563
FT	DOMAIN	565	600
FT	DOMAIN	602	638

FT	DOMAIN	640	EGF-LIKE 17.
FT	DOMAIN	675	EGF-LIKE 18.
FT	DOMAIN	713	EGF-LIKE 19.
FT	DOMAIN	750	EGF-LIKE 20.
FT	DOMAIN	788	EGF-LIKE 21.
FT	DOMAIN	826	EGF-LIKE 22.
FT	DOMAIN	866	EGF-LIKE 23.
FT	DOMAIN	904	EGF-LIKE 24.
FT	DOMAIN	942	EGF-LIKE 25.
FT	DOMAIN	980	EGF-LIKE 26.
FT	DOMAIN	1018	EGF-LIKE 27.
FT	DOMAIN	1056	EGF-LIKE 28.
FT	DOMAIN	1094	EGF-LIKE 29.
FT	DOMAIN	1142	EGF-LIKE 30.
FT	DOMAIN	1180	EGF-LIKE 31.
FT	DOMAIN	1218	EGF-LIKE 32.
FT	DOMAIN	1264	EGF-LIKE 33.
FT	DOMAIN	1304	EGF-LIKE 34.
FT	DOMAIN	1346	EGF-LIKE 35.
FT	DOMAIN	1383	EGF-LIKE 36.
FT	DOMAIN	1424	3 X LIN/NOTCH REPEATS.
FT	DOMAIN	1441	LIN/NOTCH 1.
FT	REPEAT	1478	LIN/NOTCH 2.
FT	REPEAT	1479	LIN/NOTCH 3.
FT	REPEAT	1520	6 X ANK MOTIF REPEATS.
FT	REPEAT	1521	BY SIMILARITY.
FT	DOMAIN	1871	BY SIMILARITY.
FT	DISULFID	22	BY SIMILARITY.
FT	DISULFID	29	BY SIMILARITY.
FT	DISULFID	45	BY SIMILARITY.
FT	DISULFID	47	BY SIMILARITY.
FT	DISULFID	56	BY SIMILARITY.
FT	DISULFID	62	BY SIMILARITY.
FT	DISULFID	74	BY SIMILARITY.
FT	DISULFID	87	BY SIMILARITY.
FT	DISULFID	98	BY SIMILARITY.
FT	DISULFID	106	BY SIMILARITY.
FT	DISULFID	117	BY SIMILARITY.
FT	DISULFID	128	BY SIMILARITY.
FT	DISULFID	130	BY SIMILARITY.
FT	DISULFID	139	BY SIMILARITY.
FT	DISULFID	145	BY SIMILARITY.
FT	DISULFID	150	BY SIMILARITY.
FT	DISULFID	165	BY SIMILARITY.
FT	DISULFID	176	BY SIMILARITY.
FT	DISULFID	183	BY SIMILARITY.
FT	DISULFID	194	BY SIMILARITY.
FT	DISULFID	203	BY SIMILARITY.
FT	DISULFID	214	BY SIMILARITY.
FT	DISULFID	221	BY SIMILARITY.
FT	DISULFID	232	BY SIMILARITY.
FT	DISULFID	242	BY SIMILARITY.
FT	DISULFID	253	BY SIMILARITY.
FT	DISULFID	271	BY SIMILARITY.
FT	DISULFID	280	BY SIMILARITY.
FT	DISULFID	282	BY SIMILARITY.
FT	DISULFID	291	BY SIMILARITY.
FT	DISULFID	305	BY SIMILARITY.
FT	DISULFID	320	BY SIMILARITY.
FT	DISULFID	331	BY SIMILARITY.
FT	DISULFID	349	BY SIMILARITY.
FT	DISULFID	358	BY SIMILARITY.
FT	DISULFID	360	BY SIMILARITY.
FT	DISULFID	369	BY SIMILARITY.
FT	DISULFID	375	BY SIMILARITY.
FT	DISULFID	380	BY SIMILARITY.
FT	DISULFID	397	BY SIMILARITY.
FT	DISULFID	408	BY SIMILARITY.
FT	DISULFID	428	BY SIMILARITY.
FT	DISULFID	437	BY SIMILARITY.
FT	DISULFID	448	BY SIMILARITY.
FT	DISULFID	455	BY SIMILARITY.
FT	DISULFID	466	BY SIMILARITY.
FT	DISULFID	475	BY SIMILARITY.
FT	DISULFID	486	BY SIMILARITY.
FT	DISULFID	493	BY SIMILARITY.
FT	DISULFID	504	BY SIMILARITY.
FT	DISULFID	513	BY SIMILARITY.
FT	DISULFID	524	BY SIMILARITY.
FT	DISULFID	531	BY SIMILARITY.
FT	DISULFID	542	BY SIMILARITY.
FT	DISULFID	551	BY SIMILARITY.
FT	DISULFID	562	BY SIMILARITY.
FT	DISULFID	569	BY SIMILARITY.
FT	DISULFID	574	BY SIMILARITY.
FT	DISULFID	588	BY SIMILARITY.
FT	DISULFID	599	BY SIMILARITY.
FT	DISULFID	606	BY SIMILARITY.
FT	DISULFID	617	BY SIMILARITY.
FT	DISULFID	626	BY SIMILARITY.
FT	DISULFID	637	BY SIMILARITY.

FT	DISULFID	644	654	BY SIMILARITY.
FT	DISULFID	649	663	BY SIMILARITY.
FT	DISULFID	665	674	BY SIMILARITY.
FT	DISULFID	681	692	BY SIMILARITY.
FT	DISULFID	686	701	BY SIMILARITY.
FT	DISULFID	703	712	BY SIMILARITY.
FT	DISULFID	719	729	BY SIMILARITY.
FT	DISULFID	724	738	BY SIMILARITY.
FT	DISULFID	740	749	BY SIMILARITY.
FT	DISULFID	756	767	BY SIMILARITY.
FT	DISULFID	761	776	BY SIMILARITY.
FT	DISULFID	778	787	BY SIMILARITY.
FT	DISULFID	794	805	BY SIMILARITY.
FT	DISULFID	799	814	BY SIMILARITY.
FT	DISULFID	816	825	BY SIMILARITY.
FT	DISULFID	832	843	BY SIMILARITY.
FT	DISULFID	837	854	BY SIMILARITY.
FT	DISULFID	856	865	BY SIMILARITY.
FT	DISULFID	872	883	BY SIMILARITY.
FT	DISULFID	877	892	BY SIMILARITY.
FT	DISULFID	894	903	BY SIMILARITY.
FT	DISULFID	910	921	BY SIMILARITY.
FT	DISULFID	915	930	BY SIMILARITY.
FT	DISULFID	932	941	BY SIMILARITY.
FT	DISULFID	966	977	BY SIMILARITY.
FT	DISULFID	991	1006	BY SIMILARITY.
FT	DISULFID	1008	1017	BY SIMILARITY.
FT	DISULFID	1024	1035	BY SIMILARITY.
FT	DISULFID	1029	1044	BY SIMILARITY.
FT	DISULFID	1046	1055	BY SIMILARITY.
FT	DISULFID	1062	1073	BY SIMILARITY.
FT	DISULFID	1067	1082	BY SIMILARITY.
FT	DISULFID	1084	1093	BY SIMILARITY.
FT	DISULFID	1100	1121	BY SIMILARITY.
FT	DISULFID	1115	1130	BY SIMILARITY.
FT	DISULFID	1132	1141	BY SIMILARITY.
FT	DISULFID	1148	1159	BY SIMILARITY.
FT	DISULFID	1153	1168	BY SIMILARITY.
FT	DISULFID	1170	1179	BY SIMILARITY.
FT	DISULFID	1186	1197	BY SIMILARITY.
FT	DISULFID	1191	1206	BY SIMILARITY.
FT	DISULFID	1208	1217	BY SIMILARITY.
FT	DISULFID	1224	1243	BY SIMILARITY.
FT	DISULFID	1237	1252	BY SIMILARITY.
FT	DISULFID	1254	1263	BY SIMILARITY.
FT	DISULFID	1270	1283	BY SIMILARITY.
FT	DISULFID	1295	1292	BY SIMILARITY.
FT	DISULFID	1294	1303	BY SIMILARITY.
FT	DISULFID	1310	1321	BY SIMILARITY.
FT	DISULFID	1315	1333	BY SIMILARITY.
FT	DISULFID	1335	1344	BY SIMILARITY.
FT	DISULFID	1351	1362	BY SIMILARITY.
FT	DISULFID	1356	1371	BY SIMILARITY.
FT	DISULFID	1373	1382	BY SIMILARITY.
FT	DISULFID	1390	1401	BY SIMILARITY.
FT	DISULFID	1395	1412	BY SIMILARITY.
FT	DISULFID	1414	1423	BY SIMILARITY.
FT	DISULFID	1462	1462	POTENTIAL.
FT	CARBOHYD	887	887	POTENTIAL.
FT	CARBOHYD	958	958	POTENTIAL.
FT	CARBOHYD	1178	1178	POTENTIAL.
FT	CARBOHYD	1487	1487	POTENTIAL.
FT	CARBOHYD	1508	1508	POTENTIAL.
FT	CARBOHYD	1584	1584	POTENTIAL.
SO	SEQUENCE	2524 AA;	275123 MM;	E63584B1 CRC32;

Query Match 4.6%; Score 108; DB 1; Length 2524;

Best Local Similarity 15.2%; Pred. No. 6.55e-04;

Matches 25; Conservative 21; Mismatches 108; Indels 10; Gaps 1;

Db 1149 SPNCGNATCTDITDLGSCCVAGHYGVC-SEINECUSHPCGNGCTCIDLINTYKCS 1007

Oy 49 AXXXCAEXXKCSXYRFLR-OCXAGXXNXTLXAGXEXXXXXXXCXAXEXLXSSLYDCK 107

Query Match 85.1%; Score 1781; DB 1; Length 463;
 Best Local Similarity 54.0%; Pred. No. 0.00e+00;
 Matches 248; Conservative 10; Mismatches 188; Indels 13; Gaps 4;

DB 16 TLRSLASPSSPOGSELHGRNPVDVAVNELCAAESCSRRYRLROCLAGDRMTML-- 73
 17 TLXSLXPLXLLXSSXXXRXDXAXXCAEXXCSXXRTLRQCAAGXAXXNXX 76
 DB 74 ---ANEQCAALVLEQSLYDCCRCKRGKKELOCLQIYWSHLGLTBESEYEAPVE- 129
 77 XXXAXXECXAXEXLXSSLYDCRCRGMKEXCLXITYSXHXXLXGXNXXLEXSPYEX 136
 DB 130 PVTSLRSLDIFRLASIFSGADPVVSAKSNHCLDAKACNLNDNCKRLSSYISCNREI 189
 137 PVTSLRSLDIFRLXSSXXXSXSSXXXNCLDAKACNLNDCKRLSATIYXCCXXX 196
 DB 190 SPTERCNRRKCHKALROFFDVPSEYTYRMLFCSCQ--DQACERRROTILPSCSYEDKE 247
 197 SXEXERCNRRKCHKALROFFDVPSEYTYRMLFCSCQ--DQACERRROTILPSCSYEDKE 256
 DB 248 KNCCLDLRLCTDHLCHRLADFHANCASTRITSCPADNYQACLSYAGMIFDMP 307
 257 XNCLDLRLCTDHLCHRLADFHANCASTRITSCPADNYQACLSYAGMIFDMP 316
 DB 308 NVDSNPTGIVSPMNCNCGSGNMECEKFLKDFTEPNCLNATOANGNDVAMSPRG 367
 317 NVDSNPTGIVSPMNCNCGSGNMECEKFLKDFTEPNCLNATOANGNDVAMSPRG 376
 DB 368 PTFSAQAP----RVEKTPSLPDDLSDTSLGTSTVITTCSTIQDQKANNKELSMCF 422
 377 PTFSAQAP----RVEKTPSLPDDLSDTSLGTSTVITTCSTIQDQKANNKELSMCF 436
 DB 433 TELTINISPGSKVYKILXSGCRALSTALTAPLMT 461
 437 XXXXXXXXXXXXXXXXXXXXXXXXSLXLLPVLMT 475

RESULT 2
 ID GDNF RAT STANDARD: PRT: 468 AA.
 AC 062997;
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (GDF-BETA RELATED
 DE NEUROTHROPIC FACTOR RECEPTOR 1) (RET LIGAND 1).
 DE GDFAL OR GDNFR OR TRNRI OR RETLI.
 DE RATIUS NORVEGICUS (RAT).
 DE EUDAROTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 DE EUTHERIA; RODENTIA.
 RN [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE-RETINA.
 RC MEDLINE: 96270513.
 RA JING S., WEN D., YU Y., HOLST P.-L., LUO Y., FANG M., TAMIR R.,
 RA ANTONIO L., HU Z., CUPPLES R., LOUIS J.-C., HU S., ALTROCK B.W.,
 RA FOX G.M.;
 RA CELL 85:1113-1124(1996).
 RL [2]
 RP SEQUENCE FROM N.A.
 RP STRAIN-WISTAR; TISSUE-KIDNEY;
 RC MEDLINE: 973232356.
 RA SANICOLA M., HESSION C.A., WORLEY D.S., CARMILLO P., EHRENFELS C.,
 RA MAUS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,
 RA PEPIRSKY R.B., CATE R.L.;
 RA PROC. NATL. ACAD. SCI. U.S.A. 94:6238-6243(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RP TREANOR J.J.S., GOOGMAN L., DE SAUVAGE F., STONE D.M., POULSEN K.T.,
 RA BECK C.D., GRAY C., ARANANI M.P., POLLOCK R.A., HETTI F.,
 RA PHILLIPS H.S., GODDARD A., MOORE M.W., BUJ-BELLO A., DAVIES A.M.,
 RA ASAI N., TAKAHASHI M., VANDLEN R., HENDERSON C.E., ROSENTHAL A.;

RL NATURE 382:80-83(1996).
 CC -1- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED
 CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR.
 CC -1- SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE THOUGHT TO FORM A COMPLEX
 CC WITH THE DISULFIDE-LINKED GDNF DIMER AND WITH 2 MOLECULES OF RET.
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER, BRAIN AND KIDNEY.
 CC -1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.
 DR EMBL: U59486; G139863; -;
 DR EMBL: U97142; G282022; -;
 KW RECEPTOR; GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL.
 FT SIGNAL 1 24
 FT CHAIN 25 430
 FT PROPEP 431 468
 FT DOMAIN 362 369
 FT CARBOHYD 59 59
 FT CARBOHYD 347 347
 FT CARBOHYD 406 406
 FT LIPID 430 430
 SQ SEQUENCE 468 AA; 51649 MW; 6A7A2B2A CRC32;

Query Match 85.0%; Score 1779; DB 1; Length 468;
 Best Local Similarity 50.7%; Pred. No. 0.00e+00;
 Matches 241; Conservative 12; Mismatches 213; Indels 9; Gaps 8;

DB 3 LATIYFLLPLDILMSAEVSGGDRDCVKAASDCLKBSQSTYRRLROCVAGKETNFSL 62
 15 LXTLSLXPLXLLXSSXXXRXDXAXXCAEXXCSXXRTLRQCAAGXAXXNXX 74
 DB 63 TSGLEANDCRSANEALOKSLYNCRCRGMKEXCLXITYSXHXXLXGXNXXLEXSPY 121
 75 XXXAXXECXAXEXLXSSLYDCRCRGMKEXCLXITYSXHXXLXGXNXXLEXSPY 134
 DB 122 E-PVNSRLSDIFRAVPIPSDVOVEHISGNKNCCLDAKACNLNDCKKRSAYITPCT 180
 135 EXPVTSRLSDIFRAVPIPSDVOVEHISGNKNCCLDAKACNLNDCKKRSAYITPCT 194
 DB 181 SMSN-EVCNRRKCHKALROFFDVPSEYTYRMLFCSCQ--DIACERRROTILPSCSYEE 237
 195 SXEXERCNRRKCHKALROFFDVPSEYTYRMLFCSCQ--DIACERRROTILPSCSYEE 254
 DB 238 RERNCLSLDSCCKTNYICRSLADFTNCPQPSRSNCKENYADCLLAYSGLIGTVM 297
 255 XEAPNCLDLRLCTDHLCHRLADFHANCASTRITSCPADNYQACLSYAGMIFDMP 314
 DB 298 TPNTVDS-SLS-VAPWCDSCSNGNLEDCLEKLFNFKDTCLKNAIOAFNGSDVTMNO 355
 315 TPNTVDS-SLS-VAPWCDSCSNGNLEDCLEKLFNFKDTCLKNAIOAFNGSDVTMNO 374
 DB 356 PAPPVOTTTATTTAFRVRNKP-LGPAGSENEIP-THVLPACANLQAKLSNVSGSTHL 413
 375 XXPVOTTTATTTAFRVRNKP-LGPAGSENEIP-THVLPACANLQAKLSNVSGSTHL 434
 DB 414 CLSDSDRGKGLAGASSHITTKSMAPPSCSLSLVMLTALALLSLATS 468
 435 CXAXXAXXAXXAXXAXXAXXAXXAXXAXXAXXAXXAXXAXXAXXAXXAXXAXX 489

RESULT 3
 ID NTRR HUMAN STANDARD: PRT: 464 AA.
 AC 000451;
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE NEUTRIN RECEPTOR ALPHA PRECURSOR (NTRN-ALPHA) (NTRN-ALPHA) (TGF-
 DE BETA RELATED NEUROTHROPIC FACTOR RECEPTOR 2) (GDNF RECEPTOR BETA)
 DE (GDNFR-BETA).
 DE GFA2 OR GDNFR OR TRNR2.
 OS HOMO SAPIENS (HUMAN).
 OC EUDAROTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]

ID	GENE	PROTEIN	SEQUENCE	SCORE	DB 1	DB 2	DB 3	DB 4	DB 5	DB 6	DB 7	DB 8	DB 9	DB 10	DB 11	DB 12	DB 13	DB 14	DB 15	DB 16	DB 17	DB 18	DB 19	DB 20	DB 21	DB 22	DB 23	DB 24	DB 25	DB 26	DB 27	DB 28	DB 29	DB 30	DB 31	DB 32	DB 33	DB 34	DB 35	DB 36	DB 37	DB 38	DB 39	DB 40	DB 41	DB 42	DB 43	DB 44	DB 45	DB 46	DB 47	DB 48	DB 49	DB 50	DB 51	DB 52	DB 53	DB 54	DB 55	DB 56	DB 57	DB 58	DB 59	DB 60	DB 61	DB 62	DB 63	DB 64	DB 65	DB 66	DB 67	DB 68	DB 69	DB 70	DB 71	DB 72	DB 73	DB 74	DB 75	DB 76	DB 77	DB 78	DB 79	DB 80	DB 81	DB 82	DB 83	DB 84	DB 85	DB 86	DB 87	DB 88	DB 89	DB 90	DB 91	DB 92	DB 93	DB 94	DB 95	DB 96	DB 97	DB 98	DB 99	DB 100	DB 101	DB 102	DB 103	DB 104	DB 105	DB 106	DB 107	DB 108	DB 109	DB 110	DB 111	DB 112	DB 113	DB 114	DB 115	DB 116	DB 117	DB 118	DB 119	DB 120	DB 121	DB 122	DB 123	DB 124	DB 125	DB 126	DB 127	DB 128	DB 129	DB 130	DB 131	DB 132	DB 133	DB 134	DB 135	DB 136	DB 137	DB 138	DB 139	DB 140	DB 141	DB 142	DB 143	DB 144	DB 145	DB 146	DB 147	DB 148	DB 149	DB 150	DB 151	DB 152	DB 153	DB 154	DB 155	DB 156	DB 157	DB 158	DB 159	DB 160	DB 161	DB 162	DB 163	DB 164	DB 165	DB 166	DB 167	DB 168	DB 169	DB 170	DB 171	DB 172	DB 173	DB 174	DB 175	DB 176	DB 177	DB 178	DB 179	DB 180	DB 181	DB 182	DB 183	DB 184	DB 185	DB 186	DB 187	DB 188	DB 189	DB 190	DB 191	DB 192	DB 193	DB 194	DB 195	DB 196	DB 197	DB 198	DB 199	DB 200	DB 201	DB 202	DB 203	DB 204	DB 205	DB 206	DB 207	DB 208	DB 209	DB 210	DB 211	DB 212	DB 213	DB 214	DB 215	DB 216	DB 217	DB 218	DB 219	DB 220	DB 221	DB 222	DB 223	DB 224	DB 225	DB 226	DB 227	DB 228	DB 229	DB 230	DB 231	DB 232	DB 233	DB 234	DB 235	DB 236	DB 237	DB 238	DB 239	DB 240	DB 241	DB 242	DB 243	DB 244	DB 245	DB 246	DB 247	DB 248	DB 249	DB 250	DB 251	DB 252	DB 253	DB 254	DB 255	DB 256	DB 257	DB 258	DB 259	DB 260	DB 261	DB 262	DB 263	DB 264	DB 265	DB 266	DB 267	DB 268	DB 269	DB 270	DB 271	DB 272	DB 273	DB 274	DB 275	DB 276	DB 277	DB 278	DB 279	DB 280	DB 281	DB 282	DB 283	DB 284	DB 285	DB 286	DB 287	DB 288	DB 289	DB 290	DB 291	DB 292	DB 293	DB 294	DB 295	DB 296	DB 297	DB 298	DB 299	DB 300	DB 301	DB 302	DB 303	DB 304	DB 305	DB 306	DB 307	DB 308	DB 309	DB 310	DB 311	DB 312	DB 313	DB 314	DB 315	DB 316	DB 317	DB 318	DB 319	DB 320	DB 321	DB 322	DB 323	DB 324	DB 325	DB 326	DB 327	DB 328	DB 329	DB 330	DB 331	DB 332	DB 333	DB 334	DB 335	DB 336	DB 337	DB 338	DB 339	DB 340	DB 341	DB 342	DB 343	DB 344	DB 345	DB 346	DB 347	DB 348	DB 349	DB 350	DB 351	DB 352	DB 353	DB 354	DB 355	DB 356	DB 357	DB 358	DB 359	DB 360	DB 361	DB 362	DB 363	DB 364	DB 365	DB 366	DB 367	DB 368	DB 369	DB 370	DB 371	DB 372	DB 373	DB 374	DB 375	DB 376	DB 377	DB 378
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DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF-BETA RELATED
 NEUROTROPHIC FACTOR RECEPTOR 1).
 GN GFRAL OR GDNFR ALPHA OR TRHR1.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=DORSAL ROOT GANGLION;
 RA MYOTUBE K.;
 RL SUBMITTED (FEB-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED
 CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.
 DR EMBL: AB008000; G1816442; -.
 KM MGI:1100842; GFRAL.
 KW RECEPTOR; GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL.
 FT SIGNAL 1 24
 FT CHAIN 25 430
 FT PROPEP 431 468
 FT DOMAIN 362 369
 FT CARBOHYD 59
 FT CARBOHYD 347 347
 FT CARBOHYD 406 406
 FT LIPID 430 430
 SQ SEQUENCE 468 AA; 51782 MW; 6C64C182 CRC32;
 Query Match 84.2%; Score 1762; DB 1; Length 468;
 Best Local Similarity 49.7%; Pred. No. 0.00e+00;
 Matches 226; Conservative 19; Mismatches 211; Indels 9; Gaps

ID GDNF_HUMAN STANDARD: PRT: 464 AA.
 AC P56159;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF-BETA RELATED
 DE NEUROTROPHIC FACTOR RECEPTOR 1).
 GN GFRAL OR GDNFRA OR TRNRI.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
 OC EUTHERIA: PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-SUBSTANTIA NIGRA;
 RX MEDLINE: 96270513.
 RA JING S., WEN D., YU Y., HOLST P.L., LUO Y., FANG M., TAMIR R.,
 RA ANTONIO L., HU Z., CUPPLES R., LOUIS J.-C., HU S., ALTROCK B.W.,
 RA FOX G.M., HU Z., CUPPLES R., LOUIS J.-C., HU S., ALTROCK B.W.,
 RA CELL 83:1113-1124(1996).
 CC -1- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED
 CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR (BY
 CC SIMILARITY).
 CC -1- SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE THOUGHT TO FORM A COMPLEX
 CC WITH THE DISULFIDE-LINKED GDNF DIMER AND 2 MOLECULES OF RET (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.
 CC DR MIM: 601496; -.
 CC KW RECEPTOR: GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL.
 CC FT SIGNAL 1 24
 CC FT CHAIN 25 428 GDNF RECEPTOR ALPHA.
 CC FT PROPEP 429 464 HYDROPHOBIC, REMOVED DURING MATURATION
 CC FT DOMAIN 361 368 POTENTIAL.
 CC FT CARBOHYD 59 59 POTENTIAL.
 CC FT CARBOHYD 346 346 POTENTIAL.
 CC FT CARBOHYD 405 405 POTENTIAL.
 CC FT LIPID 428 428 GPI-ANCHOR (POTENTIAL).
 CC SQ SEQUENCE 464 AA; 51291 MW; 2683574 CRC32;.

Query Match 81.1%; Score 1696; DB 1; Length 464;
 Best Local Similarity 49.7%; Pred. No. 0.00e+00;
 Matches 236; Conservative 16; Mismatches 210; Indels 13; Gaps 11;

Db 3 LATVFAFLPLDLILSAEVSQSDRLDVCVAKASQCLKEOSCSKRYTLNQCAAGKETSFL 62
 15 LXTLXSLXPLXLLXAXXXXXXXDXVAXXXCAEXXCSXXRTLRQCAAGXXXXXX 74
 Db 63 ASGLEAKDECRSAMBLKOKSLYNCRCRGMKEKNCRLIYWSMTQSLQ-GNDLLESPY 121
 75 XXXXXAXXEXXAXXEXXSLYDCRCRGMKEKNCRLIYWSMTQSLQ-GNDLLESPY 134
 Db 122 E-PVNSRLSDIFRVPVPSIDVFQOYEHIPIKGNCLDAKACNLNDICKKRSAYITPCTT 180
 135 EXPVTSRLSDIFRXXSXXSXXSXXSXXSXXSXXSXXSXXSXXSXXSXXSXXSXXSXX 194
 Db 181 SVSN-DVNCNRKCHKALROFDDKVPARHSYGLFCSCG--DIATERROQITIVVCYEE 237
 195 XXSXXKERCNRKCHKALROFDDKVPARHSYGLFCSCGXXSXXSXXSXXSXXSXXSXXSXX 254
 Db 238 REKNCL-LQDSCKNTYICRSRLADFTNCPESRSVSSCLKENYACDLAYSGLIGTVM 296
 255 XEXPNCLDLSRXCRTDLKCRSLADFTNCPXRXRXRXRXRXRXRXRXRXRXRXRXRXRXRX 314
 Db 297 TPNVDS-SLS-VAPDCDSNSGNDLECKLFLNFRDNTCLMAIQAENGSDVTVMQ 354
 315 TPNVDSXXVAVPCXGSGNXXECEKFLXFXNPNCLNAIQAENGSDVTVMQ 374
 Db 355 PAPVOTTTATTTALRVKKRP-LGPAENSELP-THVLPCCANLQAKLSVSGTTL 412
 375 XXPVOTTTATTTALRVKKRP-LGPAENSELP-THVLPCCANLQAKLSVSGTTL 434

Db 413 CINSNGVEKGLGASSHITK-SMAAPSCGLSPVLVLTALSTLLS--LTETS 464
 435 CAXXXXXXXXXXXXXXXXXXXXXXAXXSLXLPVLMFLXLLXLLXLLXLLXLLXLLXLLX 489

RESULT 6
 ID NRTNR-CHICK STANDARD: PRT: 465 AA.
 AC O13157;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE NEURTURIN RECEPTOR ALPHA PRECURSOR (NTRN-ALPHA) (GDNF
 DE RECEPTOR BETA) (GDNFR-BETA).
 GN GFR2 OR GDNFRB.
 OS GALUS GALLUS (CHICKEN).
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: AVES; NEOGNATHAE;
 OC GALIIFORMES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX BU-BELLO A., ADU J., PINON L.G.P., HORTON A., THOMPSON J.,
 RA ROSENTHAL A., CHINCETRU M., BUCHMAN V.L., DAVIES A.M.;
 RA NATURE 387:721-724(1997).
 CC -1- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NRTN-INDUCED
 CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR. ALSO ABLE
 CC TO MEDIATE GDNF SIGNALING (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.
 CC DR EMBL: U90542; G221805; -.
 CC KW RECEPTOR: GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL.
 CC FT SIGNAL 1 21
 CC FT CHAIN 22 445 NEURTURIN RECEPTOR ALPHA.
 CC FT PROPEP 446 465 HYDROPHOBIC, REMOVED DURING MATURATION
 CC FT CARBOHYD 355 355 POTENTIAL.
 CC FT CARBOHYD 387 387 POTENTIAL.
 CC FT CARBOHYD 412 412 POTENTIAL.
 CC FT LIPID 445 445 GPI-ANCHOR (POTENTIAL).
 CC SQ SEQUENCE 465 AA; 51908 MW; 5CA073E4 CRC32;.

Query Match 76.8%; Score 1607; DB 1; Length 465;
 Best Local Similarity 47.1%; Pred. No. 0.00e+00;
 Matches 218; Conservative 33; Mismatches 196; Indels 16; Gaps 11;

Db 16 TLNSLAPSPSPGDDLGWVFPVYDCIRANKLCAEGSCSSRYRTLROCLAGRDRNTML-- 73
 17 TLNSLAPSPSPGDDLGWVFPVYDCIRANKLCAEGSCSSRYRTLROCLAGRDRNTML-- 75
 Db 74 ---ANKCCQALAEVLOEPLDYDCRCRGMKEKNCRLIYWSMTQSLQ-GNDLLESPY 121
 77 XXXXXAXXEXXAXXEXXSLYDCRCRGMKEKNCRLIYWSMTQSLQ-GNDLLESPY 134
 Db 130 PITSRLSDIFRLASIFSGM--DPATNSKSNHCLDAKACNLNDICKKRSAYITPCTT 180
 137 PVSRLSDIFRXXSXXSXXSXXSXXSXXSXXSXXSXXSXXSXXSXXSXXSXXSXX 194
 Db 188 SATEHCSRRKCHKALROFDDKVPARHSYGLFCSCG--DOCAEPRTQITIVVCYEE 237
 197 SXKERCNRKCHKALROFDDKVPARHSYGLFCSCGXXSXXSXXSXXSXXSXXSXXSXX 256
 Db 246 KPNCLDLRNVCRADHLKCRSLADFTNCPESRSVSSCLKENYACDLAYSGLIGTVM 296
 257 XPNCLDLRNVCRADHLKCRSLADFTNCPXRXRXRXRXRXRXRXRXRXRXRXRXRXRXRX 314
 Db 306 NYDASTSITLSPWCSGSGNLECEKFLRDLFENCLNNAIQAENGSDVTVMQ 354
 317 NYDASTSITLSPWCSGSGNLECEKFLRDLFENCLNNAIQAENGSDVTVMQ 374
 Db 366 PSEPTTM--LPVYKSPALPD-DINDSNTMYD-TSITITCTSIQHGKLNKSKOSQSLCY 421
 377 PXXXTTAXXAXXAXXAXXAXXAXXAXXAXXAXXAXXAXXAXXAXXAXXAXXAXXAXX 436

DB 422 SETQLTDMPOKTFVDKAGSRHRAARILPAVPILKIL 464
 QY 437 XXXXXXXXXXXXXXXXXXXXXXXX-5XXLXLPVILMTXL 477

RESULT 7
 ID GDNF CHICK STANDARD: PRT: 469 AA.
 AC 013156;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF-BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 1).
 GN GFRAL OR GDNFR.
 OS GALUS GALLUS (CHICKEN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE; GALLIFORMES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA BOU-BELLO A., ADU J., PINON L.G.P., HORTON A., THOMPSON J., ROSENTHAL A., CHINCETRU M., BUCHMAN V.L., DAVIES A.M.;
 RL NATURE 387:721-724(1997).
 CC -1- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR (BY SIMILARITY).
 CC -1- SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE THOUGHT TO FORM A COMPLEX WITH THE DISULFIDE-LINKED GDNF DIMER AND WITH 2 MOLECULES OF RET (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY SIMILARITY). BELONGS TO THE GDNFR FAMILY.
 CC EMBL: U90541; G2213803;
 DR RECEPTOR: GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL.
 KW STGNAL 1 27
 FT CHAIN 28 430
 FT PROPER 431 469
 FT DOMAIN 361 368
 FT CARBOHYD 62 62
 FT CARBOHYD 163 163
 FT CARBOHYD 346 346
 FT CARBOHYD 405 405
 FT LIPID 430 430
 SQ SEQUENCE 469 AA; 52043 MM; C8D241C9 CRC32;

Query Match 72.7%; Score 1521; DB 1; Length 469;
 Best Local Similarity 45.2%; Pred. No. 0.00e+00;
 Matches 212; Conservative 23; Mismatches 219; Indels 15; Gaps 12;

DB 6 LYLALPLADVLSAVSLPBGDRLDCKYKASDOCLKESGCTKRYRTLRQCVAKESPSR 65
 QY 15 LXTLSLXXPLXAXXXXXXXVAXXKCAEXKXKXRTLLKQCAAGAXXNXX 74

DB 66 ATGLEAKDECKSAMKALOKSLYNCRCRGMKKEKNCRIYMSYOSIQ-GNDLEDESPY 124
 QY 75 XXXXXXXXKAXXKXSLYDRCRGMKKEKNCRIYMSYOSIQXXXXXLESPY 134

DB 125 E-PVNSRLSDIFRLAPIVS---EPVLS-KNNCLDAKACNLDTCRFRSAVITPPTS 179
 QY 135 EXPVTSRLSDIFRAXXSSXXSXKXKXNXCDAKACNLDXCKRLRSAYIXKXX 194

DB 180 STSN-EICNKRKCHALFLFDKVPKHSYGMTCSCR--DVACERRRQTIIVPCSYED 236
 QY 195 XXXXKERNRRCHALQFFDKVPKHXHXYGLFSCXXXDXACKERRRQTIIVPCSYEX 254

DB 237 REKPCMLIOESCKKNYICRSRLADFTNCOPESSRSVSSCKENYADCLAYSGILGIVM 296
 QY 255 XEPRICDLRSKCRDXLCRSLADFTNCOPESSRSVSSCKENYADCLAYSGILGIVM 314

DB 297 TPNYIDSS-SLS-VAPMCDGNSGNDIDECRKFLEFODNTGCLKNAIDAFNGDIDVNWQ 354
 QY 315 TPNYIDSSXXTXVAPMCDGNSGNDIDECRKFLEFODNTGCLKNAIDAFNGDIDVNWQ 374

DB 355 PILVOTTAATTTASRLKNTGETTNEIPTHNSPACAN-LQAKRR-KSNESVDTEL 412
 QY 375 XXPXXXXXXAXXXXXXXRXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 434

DB 413 CLNENAGKNDPTGVSTSHISENSFALPTSFYPSPLILMTALSFL 461
 QY 435 CXXXXXXXKX 481

RESULT 8
 ID NOTC_XENLA STANDARD: PRT: 2524 AA.
 AC P21783;
 DT 01-MAY-1991 (REL. 18, CREATED)
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG PRECURSOR (NOTCH PROTEIN).
 GN NOTCH.
 OS XENOPUS LAEVIS (AFRICAN CLAWED FROG).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 90385285.
 RA COFFMAN C., HARRIS W., KINTNER C.;
 RL SCIENCE 249:1438-1441(1990).
 RN [2]
 RP REVISIONS TO 1759-1782.
 RA KINTNER C.;
 RL SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDSI DATA BANKS.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED ALMOST UNIFORMLY IN EARLY EMBRYOS.
 CC -1- SIMILARITY: HIGH, WITH OTHER NOTCH-TYPE PROTEINS.
 CC -1- SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 3 LTV/NOTCH REPEATS.
 CC EMBL: M3874; G1364263; -;
 DR PIR: A35844; A35844.
 DR HSSP: P20693; 1ESL.
 DR PROSITE: PS00010; ASX_HYDROXYL, 23.
 DR PROSITE: PS01186; EGF_2, 29.
 DR PROSITE: PS01187; EGF_CA, 21.
 DR DIFFERENTIATION; NEUROGENESIS; REPEAT; ANK REPEAT; EGF-LIKE DOMAIN; KW TRANSMEMBRANE; SIGNAL; GLYCOPROTEIN.
 FT SIGNAL 1 19
 FT CHAIN 20 2524
 FT DOMAIN 1729 1750
 FT DOMAIN 1751 2524
 FT DOMAIN 20 57
 FT DOMAIN 58 99
 FT DOMAIN 102 140
 FT DOMAIN 141 177
 FT DOMAIN 179 215
 FT DOMAIN 217 254
 FT DOMAIN 256 332
 FT DOMAIN 333 370
 FT DOMAIN 371 409
 FT DOMAIN 411 449
 FT DOMAIN 451 487
 FT DOMAIN 489 525
 FT DOMAIN 527 563
 FT DOMAIN 565 600
 FT DOMAIN 602 638
 FT DOMAIN 640 675
 FT DOMAIN 677 713
 FT DOMAIN 715 750
 FT DOMAIN 752 788
 FT DOMAIN 790 826
 FT DOMAIN 828 866
 FT DOMAIN 868 904
 FT DOMAIN 906 942


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FT DOMAIN 944 980 EGF-LIKE 25, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 982 1018 EGF-LIKE 26.
FT DOMAIN 1020 1056 EGF-LIKE 27, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1058 1094 EGF-LIKE 28.
FT DOMAIN 1096 1142 EGF-LIKE 29.
FT DOMAIN 1144 1180 EGF-LIKE 30, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1182 1218 EGF-LIKE 31, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1220 1264 EGF-LIKE 32, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 1266 1304 EGF-LIKE 33.
FT DOMAIN 1306 1346 EGF-LIKE 34.
FT DOMAIN 1347 1383 EGF-LIKE 35.
FT DOMAIN 1386 1424 EGF-LIKE 36.
FT DOMAIN 1441 1560 3 X LIN/NOTCH REPEATS.
FT REPEAT 1441 1478 LIN/NOTCH 1.
FT REPEAT 1479 1520 LIN/NOTCH 2.
FT REPEAT 1521 1560 LIN/NOTCH 3.
FT DOMAIN 1871 2083 6 X ANK MOTIF REPEATS.
FT DISULFID 22 35 BY SIMILARITY.
FT DISULFID 29 45 BY SIMILARITY.
FT DISULFID 47 56 BY SIMILARITY.
FT DISULFID 62 74 BY SIMILARITY.
FT DISULFID 68 87 BY SIMILARITY.
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FT DISULFID 130 139 BY SIMILARITY.
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FT DISULFID 1315 1333 BY SIMILARITY.
FT DISULFID 1335 1344 BY SIMILARITY.
FT DISULFID 1351 1362 BY SIMILARITY.
FT DISULFID 1366 1371 BY SIMILARITY.
FT DISULFID 1373 1382 BY SIMILARITY.
FT DISULFID 1390 1401 BY SIMILARITY.
FT DISULFID 1395 1412 BY SIMILARITY.
FT DISULFID 1414 1423 BY SIMILARITY.
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FT CARBOHYD 887 887 POTENTIAL.
FT CARBOHYD 958 958 POTENTIAL.
FT CARBOHYD 1178 1178 POTENTIAL.
FT CARBOHYD 1487 1487 POTENTIAL.
FT CARBOHYD 1508 1508 POTENTIAL.
FT CARBOHYD 1584 1584 POTENTIAL.
SQ SEQUENCE 2524 AA; 275123 MW; E63584B1 CRC32;
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Query Match 5.28; Score 109; DB 1; Length 2524;
Best Local Similarity 16.08; Pred. No. 9,728-05;
Matches 26; Conservative 18; Mismatches 109; Indels 10; Gaps 10;

Db 1149 SPNPGONAGCTDTYLGISCECVAGHGVNCSSEINECSHPGONGGTGIDINTYKGS
QY 44 AAXXXCAEXXCSXXYRFLR-QCYAGXX-NNXXXXXXAXXECXAXXEXLXXSSLYVW
Db 1209 PRG-TGVHC-EIN-VDDCPFPVDSFTLEPKCINNKCIDRUG-VNCL-CEPGFVGENC
QY 102 KRGKKEXXKLXYWSXHXHXXGXXHXXLESPEXP-VTSRLSDIFRXXSXXSXXDX
Db 1264 EGD-VNECLSNPCDSRGTONCIDLVDYRCECRGFTGR-RCE 1304
QY 161 XXXKSNXCIDAAKACNLNDXCKTLBSAITYIXKXXSXXSXXERCN 203
```

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Mpsrch_n n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Fri Mar 12 13:08:00 1999; Maspar time 2460.88 Seconds
 1236.356 Million cell updates/sec

Tabular output not generated.

Title: >US-08-866-354-41
 Description: (1-1699) from US08866354.seq
 Perfect Score: 1699

N.A. Sequence: 1 GCGCGCGCGTCGACCGAGCG.....CCACCGTCGACCGCGCGCGC 1699
 Comp: GCGCGCGCGTCGACCGTCGCG.....GCTTGCGAGCTGCGCGCGCGC

Scoring table: TABLE default
 Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 2275026 segs, 895388244 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: emb1-est56
 1:em_est1 2:em_gss1 3:em_gss2 4:em_gss3
 Database: genbank-est109
 5:gb_est1 6:gb_est10 7:gb_est11 8:gb_est12 9:gb_est13
 10:gb_est14 11:gb_est15 12:gb_est16 13:gb_est17
 14:gb_est18 15:gb_est19 16:gb_est2 17:gb_est20
 18:gb_est21 19:gb_est3 20:gb_est4 21:gb_est5 22:gb_est6
 23:gb_est7 24:gb_est8 25:gb_est9 26:gb_gss1 27:gb_gss2
 28:gb_gss3 29:gb_gss4

Statistics: Mean 11.495; Variance 2.154; scale 5.337

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	381	22.4	442	22	AA049894 mjl1d08.r1 Soares	0.00e+00
2	349	20.5	465	21	AA050083 m106d05.r1 Soares	0.00e+00
3	337	19.8	499	14	AA925330 UT-R-A1-ek-h-10-0-UT	0.00e+00
4	271	16.0	448	18	AA180186 EST223927 Normalized	0.00e+00
5	254	14.9	353	21	AA041935 m104b08.r1 Soares	0.00e+00
6	251	14.8	431	18	AA179473 EST223187 Normalized	0.00e+00
7	223	13.1	502	23	AA238748 m135d09.r1 Barstead	0.00e+00
8	128	7.5	387	20	W99197 m159f10.r1 Soares	0.00e+00
9	64	3.8	252	12	AA754459 97SN1787 Rice	5.69e-72
10	59	3.5	252	12	AA754459 97SN1787 Rice	1.66e-62
11	47	2.8	247	12	AA754458 97SN1784 Rice	1.26e-40
12	46	2.7	247	12	AA754458 97SN1784 Rice	7.20e-39
13	37	2.2	478	21	W73681 z55h01.r1 Soares	1.11e-23

14	37	2.2	2275	11	AF034173	Homo sapiens ntcon2 co	1.11e-23
15	35	2.1	350	25	AA349976	ESR56965 Infant brain	1.72e-20
16	36	2.1	2275	11	AF034173	Homo sapiens ntcon2 co	4.47e-22
17	30	1.8	205	17	AA783969	cg90781.f1 Aspergillus	6.60e-13
18	29	1.7	436	21	W69813	z48906.f1 Soares feta	1.81e-11
19	29	1.7	792	18	AU035938	Mus musculus cDNA, clo	1.81e-11
20	27	1.6	374	23	AA144007	mr75b01.f1 Stratagene	1.10e-08
21	27	1.6	409	23	AA153254	mr75b01.f1 Stratagene	1.10e-08
22	28	1.6	436	21	W69813	z48906.f1 Soares feta	4.63e-10
23	28	1.6	567	9	AA534427	nt16d11.s1 NCI_CGAP	4.63e-10
24	27	1.6	667	12	AA0110816	Cit-HSP-2372014.TR Cit	1.10e-08
25	25	1.5	1287	12	AF038250	Homo sapiens clone ntc	4.63e-10
26	25	1.5	289	21	AA080880	mw70b02.r1 Soares	4.82e-05
27	25	1.5	360	13	AA0809745	mw70b02.r1 Soares	4.82e-05
28	26	1.5	387	23	AA142537	ms07604.f1 Stratagene	2.40e-07
29	25	1.5	394	29	AA0145613	HS_3170.A1-G06_MR Cit	4.82e-06
30	26	1.5	415	13	AA839237	vw55d06.f1 Stratagene	2.40e-07
31	25	1.5	421	16	R78049	y180a08.r1 Homo sapien	2.40e-07
32	25	1.5	430	20	W76716	mb11h06.f1 Soares	4.82e-06
33	25	1.5	442	22	AA023705	ze33c03.s1 Soares feta	4.82e-06
34	25	1.5	446	6	AA587098	vc18b07.f1 KO mouse em	4.82e-06
35	25	1.5	455	8	AA524878	ng46h10.s1 NCI_CGAP	4.82e-06
36	25	1.5	457	6	AA437089	zv53a10.s1 Soares feta	4.82e-06
37	26	1.5	474	11	AA694259	z131d11.s1 Soares test	2.40e-07
38	25	1.5	490	13	AA883883	am65602.s1 Soares NFL	4.82e-06
39	26	1.5	510	17	AT091539	ow59a01.x1 Soares NSF	2.40e-07
40	26	1.5	521	7	AA530753	v14e07.f1 Stratagene	2.40e-07
41	25	1.5	566	27	FR0032477	Fugu rubripes GSS sequ	4.82e-06
42	26	1.5	631	7	AA518362	v110d02.r1 Barstead mo	2.40e-07
43	25	1.5	660	11	AF034177	Homo sapiens ntcon6 co	4.82e-06
44	24	1.4	445	7	RICS2438A	Rice cDNA, partial seq	8.83e-05
45	24	1.4	451	12	AA201294	LD04235.Sprtime LD Dros	8.83e-05

ALIGNMENTS

RESULT 1
 LOCUS AA049894 442 bp mRNA EST 30-DEC-1996
 DEFINITION mjl1d08.r1 Soares mouse embryo NBM13.5 14.5 Mus musculus cDNA
 clone 475791 5', mRNA sequence.
 ACCESSION AA049894
 NID 91755226
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 442)
 AUTHORS Marr, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Pridmore, G., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, P., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R., et al.
 TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT On Dec 31, 1996 this sequence version replaced g1:152956c.

CONTACT: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 TEL: 314 286 1800
 FAX: 314 286 1810
 EMAIL: mouseest@wustl.edu
 THIS CLONE IS AVAILABLE ROYALTY-FREE THROUGH LBNL; CONTACT THE
 IMAGE CONSORTIUM (info@image.llnl.gov) FOR FURTHER INFORMATION.
 WGI:86535
 Seq primer: -28M13 rev2 from Amerham
 High quality sequence stop: 405.
 Location/Qualifiers
 1..442
 /organism="Mus musculus"


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OY      315 CCTGTAAGCAGACAGCACTAGAGACAGCTCTCTCTATAGATGACAGTGCACAGCGG 374
DB      357 CATGAGACAGCAAGCTACTCTGTGACATTATTGGACCTTACCTGCGCCAGAGCT 416
OY      375 CATGAGACAGCAAGCTACTCTGTGACATTATTGGACCTTACCTGCGCCAGAGCT 434
DB      417 TGTGACTACGAGTTGATGTCCTACCCCTATGAAGACAGACAGTGCACAGC 465
OY      435 TGTGACTACGAGTTGATGTCCTACCCCTATGAAGACAGACAGTGCACAGC 483

RESULT  3
LOCUS   AA925330      499 bp      mRNA      EST      21-APR-1998
DEFINITION  UR-R-A1-ek-h-10-0-UI-s1 UR-R-A1 Rattus norvegicus cDNA clone
            UR-R-A1-ek-h-10-0-UI-3 similar to g112627159(db)|AB008833|AB008833
            Mus musculus mRNA for Gfra1pna-3, complete cds, mRNA sequence.
ACCESSION AA925330
NID       G3072466
KEYWORDS  EST.
SOURCE    Norway rat.
ORGANISM  Rattus norvegicus
          Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
          Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 499)
          Ronaldo, M.F., Lennon, G., and Soares, M.B.
          Normalization and subtraction: two approaches to facilitate gene
          discovery
          Genome Res. 6 (9), 791-806 (1996)
          97044477

JOURNAL  Program for Rat Gene Discovery and Mapping
MEDLINE  University of Iowa
          451 Eckstein Medical Research Building Iowa City, IA 52242, USA
          Tel: 319 335 8250
          Fax: 319 335 9565
          Email: mssoares@blue.weeg.iowa.edu

COMMENT   The sequence tag present in the cDNA between the NotI site and the
          oligo-dT track (not shown) served to identify it as a clone from
          the normalized adult kidney library. cDNA Library Preparation: M.
          Fatima Ronaldo, Ph.D. Clone distribution: clones will be available
          through Research Genetics
          Seq primer: M13 forward.

FEATURES
  source          Location/Qualifiers
    1..499
    /organism="Rattus norvegicus"
    /strain="Sprague-Dawley"
    /note="Vector: pT73D-Pac (Pharmacia) with a modified
    polylinker. Site_1: Not I; Site_2: Eco RI; The UR-R-A1
    library is a subtracted library derived from the UR-R-A0
    library. The UR-R-A0 library consisted of a mixture of
    individually tagged normalized libraries constructed from
    rat placenta, adult lung, brain, liver, kidney, heart,
    spleen, ovary, and muscle. The tag is a string of 3-5
    nucleotides present between the NotI site and the
    oligo-dT track which allows identification of the library
    of origin of a clone within the mixture. The subtracted
    library (UI-R-A1) was constructed as follows: PCR
    amplified cDNA inserts from a pool of approximately 3,840
    UI-R-A0 clones from which 3' ESTs had been derived was
    used as a driver in a hybridization with the UR-R-A0
    library in the form of single-stranded circles. The
    remaining single-stranded circles (subtracted library) was
    purified by hydroxyapatite column chromatography,
    converted to double-stranded circles and electroporated
    into DH10B bacteria (Life Technologies) to generate the
    UR-R-A1 library. This procedure has been previously
    described (Ronaldo, Lennon and Soares, genome Research 6:
    791-806, 1996)"
    /db_xref="taxon:10116"
    /clone="UR-R-A1-ek-h-10-0-UI"
    /clone_1lb="UR-R-A1"
  
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BASE COUNT 132 a 120 c 141 g 104 t 2 others
ORIGIN
Query Match 19.8%; Score 337; DB 14; Length 499;
Best Local Similarity 99.4%; Pred. No. 0.00e+00;
Matches 337; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB      161 GGTGGACACCAAGCTTCTCTCAAAAGGACCATTTTCTCAAGTGCCTCAGACCCCTC 220
CP      1685 GGTGGACACCAAGCTTCTCTCAAAAGGACCATTTTCTCAAGTGCCTCAGACCCCTC 1526
DB      221 AGCTGCTCTCTGAGAGACCAAGCAAGTATGAGTACATTCCTGGTGGTCTCT 2000
CP      1625 AGCTGCTCTCTGAGAGACCAAGCAAGTATGAGTACATTCCTGGTGGTCTCT 1526
DB      281 GGGAAACAGAGAGAGGCTGAGGTGGAGCTAATCACACCATATATACAGCCANA 1526
CP      1565 GGGAAACAGAGAGAGGCTGAGGTGGAGCTAATCACACCATATATACAGCCANA 1526
DB      341 CTGAGTACAAAGTCTCTANGAGAGACGCCAAGCAGAGTAAAGTAAAGCTTTGAA 1526
CP      1505 CTGAGTACAAAGTCTCTANGAGAGACGCCAAGCAGAGTAAAGTAAAGCTTTGAA 1526
DB      401 AGCTGGCGCTCAGATTCGAAAGGTCACAGCCCTGCTTCCAAAGCTCATCTG 450
CP      1445 AGCTGGCGCTCAGATTCGAAAGGTCACAGCCCTGCTTCCAAAGCTCATCTG 1526
DB      461 AGCAGACAGATGTGACAGTGCAGCTGTTGCATCTTCT 499
CP      1385 AGCAGACAGATGTGACAGTGCAGCTGTTGCATCTTCT 1347

RESULT  4
LOCUS   A1180186      448 bp      mRNA      EST      08-APR-1998
DEFINITION  RSPCR62 3' end, mRNA sequence.
ACCESSION A1180186
NID       G3730824
KEYWORDS  EST.
SOURCE    Rattus sp.
ORGANISM  Rattus sp.
          Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
          Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 448)
          Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J.,
          Kerlavage, A.R., and Adams, M.D.
          Rat Genome Project: Generation of a Rat EST (RESE) Catalog & Rat
          Gene Index
          Unpublished (1998)

JOURNAL  Contact: Lee, NH
MEDLINE  ATCC
          The Institute for Genomic Research
          9712 Medical Center Drive, Rockville, MD 20850, USA
          Tel: (301)-838-3529
          Fax: (301)-838-0208
          Email: nhlee@tigr.org
          Seq primer: M13-21.

FEATURES
  source          Location/Qualifiers
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    /organism="Rattus sp."
    /note="Organ: spleen; Vector: pT73Pac; Site_1: EcoRI;
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    /clone="RSPCR62"
    /clone_1lb="Normalized rat spleen, Bento Soares"
  
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Query Match 16.0%; Score 271; DB 18; Length 448;
 Best Local Similarity 98.6%; Pred. No. 0.00e+00;

[illegible]

Query Match
Best Local Similarity 88.3%; Pred. No. 0.006+00;
Matches 257; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

mRNA
BASE COUNT 94 A 157 C 122 G 129 T
ORIGIN
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/db_xref="taxon:10090"
/clone_id="Bartstead mouse pooled organs MPLRB4"
/seq="mixed"
/dev_stage="7 day"
/lab_host="DH10B"

Db 15 TGAGAGCCATTGCACGCTAAGATGGGTTCACACAGACGCTTCTCCAGGACTGGCAG 74
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|||
Oy 1082 TGAGAGCCATTGCAGCTAAATGCCGTTCCACAGACAACCTCTTCCAGGACTGGCGG 1141
|||||
|||
Db 75 ACTCACTTTTTCAGTGSTGCAGACGACGAACAGAACCCCTGCTGTAGACTGCAGGCCA 134
|||||
|||
Oy 1142 ACTCACTTTTTCGTGTATGAGACGACGACGAACAGACCCTGCTGTGAGCCCCAGCTCA 1201
|||||
|||
Db 135 GGCTACCATCTTCTTCTTCATCATCTCCCTGATTTCTGCTGCAGACCCCTGTGTAGC 194
|||||
|||
Oy 1202 GGCTACCCGCTTCTGCTTCTTCTTCACTTCTTACTTATTTCTGTGCAGACCCCTGTGTAGC 1261
|||||
|||
Db 195 TGGGCTTCCTCAGAGGCTCCTTGTCTCTCCACACACACCAGACGATGATTTGCAGCCTGTGG 254
|||||
|||
Oy 1262 TGGGCTCCCTCAGAGGCTCCTTGTCTCTCCACACACACCAGACGATGATTTGCAGCCTGTGG 1321
|||||
|||
Db 255 TGGGAGAACAATCGCCAGCCTGTGTGAGAAGACGACGCTGTACACAGCA 305
|||||
|||
Oy 1322 TGGGAGAACAATCGCTGCTCTGTGAMAAGATGCACACGACCTCACCTGCA 1372
|||||
|||

RESULT 8

LOCUS W99197 387 bp mRNA EST 16-JUL-1996
DEFINITION m599t10.r1 Soares mouse embryo NM0E13.5 14.5 Mus musculus cDNA
ACCESSION W99197
NID g1429123
KEYWORDS Est.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Euthera; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.
1 (bases 1 to 387)
Marra,M., Hallier,L., Allen,M., Bowles,M., Dietrich,N., Dubouque,T.,
Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Thelshing,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HMI Mouse EST Project
Unpublished (1996)

TITLE JOURNAL COMMENT
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63114
Tel.: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LNL: confu...
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:25315
Seq primer: ETPrimer
High quality sequence stop: 341.
Location/Qualifiers
1..387
/organism="Mus musculus"
/strain="C57BL/6J"
/note=Vector: pET73D-Pac (Pharmacia) with a modified

FEATURES
SOURCE

Query Match	7.58;	Score 128;	DB 20;	Length 387;
Best Local Similarity	82.98;	Pred. NO. 3.49e-202;		
Matches 243;	Conservative 0;	Mismatches 37;	Indels 13;	Gaps 7;

RESULT	9	17056	17057	17058	17059	17060	17061	17062	17063	17064	17065	17066	17067	17068	17069	17070	17071	17072	17073	17074	17075	17076	17077	17078	17079	17080	17081	17082	17083	17084	17085	17086	17087	17088	17089	17090	17091	17092	17093	17094	17095	17096	17097	17098	17099	17100	17101	17102	17103	17104	17105	17106	17107	17108	17109	17110	17111	17112	17113	17114	17115	17116	17117	17118	17119	17120	17121	17122	17123	17124	17125	17126	17127	17128	17129	17130	17131	17132	17133	17134	17135	17136	17137	17138	17139	17140	17141	17142	17143	17144	17145	17146	17147	17148	17149	17150	17151	17152	17153	17154	17155	17156	17157	17158	17159	17160	17161	17162	17163	17164	17165	17166	17167	17168	17169	17170	17171	17172	17173	17174	17175	17176	17177	17178	17179	17180	17181	17182	17183	17184	17185	17186	17187	17188	17189	17190	17191	17192	17193	17194	17195	17196	17197	17198	17199	17200	17201	17202	17203	17204	17205	17206	17207	17208	17209	17210	17211	17212	17213	17214	17215	17216	17217	17218	17219	17220	17221	17222	17223	17224	17225	17226	17227	17228	17229	17230	17231	17232	17233	17234	17235	17236	17237	17238	17239	17240	17241	17242	17243	17244	17245	17246	17247	17248	17249	17250	17251	17252	17253	17254	17255	17256	17257	17258	17259	17260	17261	17262	17263	17264	17265	17266	17267	17268	17269	17270	17271	17272	17273	17274	17275	17276	17277	17278	17279	17280	17281	17282	17283	17284	17285	17286	17287	17288	17289	17290	17291	17292	17293	17294	17295	17296	17297	17298	17299	17300	17301	17302	17303	17304	17305	17306	17307	17308	17309	17310	17311	17312	17313	17314	17315	17316	17317	17318	17319	17320	17321	17322	17323	17324	17325	17326	17327	17328	17329	17330	17331	17332	17333	17334	17335	17336	17337	17338	17339	17340	17341	17342	17343	17344	17345	17346	17347	17348	17349	17350	17351	17352	17353	17354	17355	17356	17357	17358	17359	17360	17361	17362	17363	17364	17365	17366	17367	17368	17369	17370	17371	17372	17373	17374	17375	17376	17377	17378	17379	17380	17381	17382	17383	17384	17385	17386	17387	17388	17389	17390	17391	17392	17393	17394	17395	17396	17397	17398	17399	17400	17401	17402	17403	17404	17405	17406	17407	17408	17409	17410	17411	17412	17413	17414	17415	17416	17417	17418	17419	17420	17421	17422	17423	17424	17425
--------	---	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------

NID g2801165

MEMBERS	EST.
SOURCE	rice.

ORGANISM Olyza sa
Eukaryot

Embryoph
Poales;

REFERENCE	1 (base)
AUTHORS	Nahm, B. H.

KLM, W.T.

TITLE	Large-sc
-------	----------

COMMENT

contact:
Department

National
Suwon, K

Tel: 82
Fax: 82

Email: m

1

```

/organism="Oryza sativa"
/cultivar="Milyang23"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Directional cDNA library inserted into lambda; Vector at 5' end with EcoRI and 3' end with Xho I; Site 3: XbaI"
/db_xref="taxon:4530"
/clone="97SN187"
/clone_id="Rice Immature Seed Lambda ZAPII cDNA library"
/tissue_type="Immature Seed"

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Query Match	3.88;	Score 64;	DB 12;	Length 252;
Best Local Similarity	11.68;	Pred. No. 5.69e-72;		
Matches	25;	Conservative 112;	Mismatches 77;	Indels 2;
			Gaps	2

Db	19	MTSYXCHENBMYWVASHAGNYMVBHNCIBERGHOCCKVNNSTMYTMCVYNNBANSGBMH	78
Oy	1471	CTTGGGCTCTCTCTCTCTAGACCTTTACTCCAGTTTGGCTGTATTTGGTGCTGAT	1530
Db	79	YWBVBNTKVDGNHTRCSRMBRVTRMAHYHDYTNCBAYNNNDYHNNBMYBVTGMCST	138
Oy	1531	TAGCTTCCACCTCCAGGCTTTCTCTGTTTCCAGAGNACACCCAGGCTATGATACCA	1590
Db	139	MMCMBYNNKCLASAMHNTSYDYKSTNNWGTBYSDXSMMHGWCSSBVKYIHTKVTSTR	198
Oy	1591	CTCATTCCTGGTGGCTCTTCCAGGAAGCAGCCTAGGGTTCTGAGGCAGCTGAGAAG	1650
Db	199	ATRSYTCVARKYVMMTKTKVYKHYHVBGCHBTD	234
Oy	1651	ATGGTCCCTTT-GTGA-GGAAGCTGGTGTCTCAAC	1684

Accession	Result	LOCUS	DEFINITION
U784460	10	AA754459	252 bp mRNA
		97SN1787	Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa
		cDNA clone 97SN1787,	mRNA sequence.

NID g2801165

NEIMONDS	ESI.
SOURCE	rice.

ORGANISM Oryza sativa
Eukaryote

Embryoph
Poales:

REFERENCE	1 (base)
ATTHORS	Nahm R H

KLE, W. F.

TITLE Large-sc

COMMENT

Contact:
Department:

National
Suwon, K

Tel: 82
Fax: 82

Email: m...

Universi

seq print

source

REFERENCE
AUTHORS
1 (bases 1 to 433)
Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Roffling, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE The Washu-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT

Contact: Wilson RK
Washu-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 650 Std Error: 0.00
Seq primer: mob. REGA+ER
High quality sequence stop: 343.

FEATURES

source
1. 433
Location/Qualifiers
/organism="Homo sapiens"
/note="Organ: heart; Vector: pT73D (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' TGTTACCAATCTGAGTGGAGGCGCGCGCATCTTTTCTTTTCTTTT 3'), double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M. Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NDHL19W."
/db_xref="taxon:9606"
/clone="344593"
/clone.lib="Soares fetal heart NDHL19W"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
complement(1..>433)
109 c 132 g 120 t
BASE COUNT
ORIGIN

Query Match 12.0%; Score 265; DB 21; Length 433;
Best Local Similarity 85.5%; Pred. No. 0.00e+00;
Matches 331; Conservative 0; Mismatches 54; Indels 2; Gaps 2;
Db 11 TGTGTCTGTGTGTCTTCATTTGTCAGGCGCTGTCTGTCTGCTACTTTCAA 70
|||||
Cp 2151 TGTGTATGCGTGTGTCTTCATTTGTCAGGCGGAGTTCATATCTGGTGTGAAG 2092
|||||
Db 71 AATCTTGTACTGCTGCCACAGCCTACAGGCTGTTCAGCATCAGACAGACCA 130
|||||
Cp 2091 AACTTTGTGCTGGGTTCCAAAGGCTCAAGGCCATCAGCATCAGAGTGGAGG 2032
|||||
Db 131 CGGTCAAGCAGCCGACGCTGTGCTGTGGGCTGTGAGTTAGTTGATCACCCTGT 190
|||||
Cp 2031 CAGTCAAGCAGCCGACGCTGTGCTGTGGGCTGTGAGTTAGTTGATCACCCTTT 1972
|||||
Db 191 TACTCCCTGGGATGATTTTGTCTGAGCTCTGTGAACACATGTTAACTTTGGAGT 250
|||||
Cp 1971 TACTCCCTGGGATGATTTTGTCTGAGCTCTGTGAACACATGTTAACTTTGGAGT 1912
|||||
Db 251 TGTGGCCTTACAGCCCTGTCTGTGAGACAGCTGACAGTGGTGTGACACTGGGCC 310
|||||
Cp 1911 TGTGGCCTTACAGCCCTGTCTGTGAGATGATGTCAGAGTGTATGACACTGG- TCCCC 1853
|||||
Db 311 AAGCTGTACTGTCTACTAGGTCATCTGGCAAGAGCGCTTCTCCACCCGAGGGCC 370
|||||
Cp 1852 AAGCTGTACTGTCTACTAGGTCATCTGGCAAGAGCTTCTCCACCCGAGGGGCC 1793
|||||
Db 371 TGGGTGTGCTGGGAGCAGAGGGGCTT 397.
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Cp 1792 TGGG-TAGCTGGAGTGAAGGGGCTTT 1767

RESULT 4
LOCUS R02135 364 bp mRNA EST 31-MAR-1995
DEFINITION Y683H05.s1 Homo sapiens cDNA clone 124377 3'.
ACCESSION R02135
NID 9751871
KEYWORDS EST.
SOURCE human clone-124377 library-Soares fetal liver spleen INFLS
vector-pT73D (Pharmacia) with a modified polylinker host-DH10B
(ampicillin resistant) primer-21n3 Rsite1-Pac I Rsite2-Eco RI
liver and spleen from a 20 week-post conception male fetus. 1st
strand cDNA was primed with a Pac I - oligo(dT) primer (5'
AAGTGAAGATATATTAAGATCTTTTCTTTTCTTTT 3'), double-stranded
cDNA was ligated to Eco RI adapters (Pharmacia), digested with
I and cloned into the Pac I and Eco RI sites of the modified pT73
vector. Library went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo.

ORGANISM

Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia
Buthria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 364)

REFERENCE

1. (bases 1 to 364)
Hillier, L., Clark, N., Dubuque, T., Elliston, R., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Mar, A.,
Parsons, J., Ritzkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, R., and
Wilson, R.
The Washu-Merck EST Project
Unpublished (1995)

TITLE The Washu-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT

Contact: Wilson RK
Washu-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
High quality sequence stops: 358
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Location/Qualifiers
1. 364
/organism="Homo sapiens"
/clone="124377"

FEATURES

source
BASE COUNT 63 a 92 c 101 g 104 t 4 others
ORIGIN
Query Match 11.8%; Score 262; DB 5; Length 364;
Best Local Similarity 85.6%; Pred. No. 0.00e+00;
Matches 310; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
Db 3 TGTGTCTGTGTGTCTTCATTTGTCAGGCGGCTGTCTGTCTGCTACTTTCAA 62
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Db 63 AATCTTGTACTGCTGCCACAGCCTACAGGCTGTTCAGCATCAGACAGACCA 122
|||||
Cp 2091 AACTTTGTGCTGGGTTCCAAAGGCTCAAGGCCATCAGCATCAGAGTGGAGG 2032
|||||
Db 123 CGGTCAAGCAGCCGACGCTGTGCTGTGGGCTGTGAGTTAGTTGATCACCCTGT 182
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Cp 2031 CAGTCAAGCAGCCGACGCTGTGCTGTGGGCTGTGAGTTAGTTGATCACCCTTT 1972
|||||
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Cp 1971 TACTCCCTGGGATGATTTTGTCTGAGCTCTGTGAACACATGTTAACTTTGGAGT 1912
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Db 243 TGTGGCCTTACAGCCCTGTCTGTGAGACAGCTGACAGTGGTGTGACACTGGGCC 302
|||||
Cp 1911 TGTGGCCTTACAGCCCTGTCTGTGAGATGATGTCAGAGTGTATGACACTGG- TCCCC 1852
|||||
Db 303 AAGCTGTACTGTCTACTAGGTCATCTGGCAAGAGCGCTTCTCCACCCGAGGGCCT 352
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Cp 1851 GGCTGTGCTGTCTACTAGGTCATCTGGCAAGAGCTTCTCCACCCGAGGGGCTT 1792

Db	181	CCATCCGATGCTCTTCTGCTCTGCGAAGATGCGCGCCCTAG	227
0y	1318	CCATCCGATGCTCTTCTGCTCTGCGAAGATGCGCGCCCTAG	1364

RESULT

7

LOCUS

MA350341

416 bp

MRNA

EST

21-Apr-1997

DEFINITION

EST57915 Infant brain Homo sapiens cDNA 5' end, mRNA sequence.

ACCESSION

MA350341

NID

g2002900

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 416)

Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brannon,R.C., Man-Well,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Georgiagen,N.S., Glocke,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Balances,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dumke,D., Feng,D.-F., Ferrite,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Melsner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruden,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M., and Venter,J.C.

TITLE

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

JOURNAL

Nature 377 (6547 Suppl), 3-174 (1995)

MEDLINE

96026280

COMMENT

Other-ESTs: EST57914 TH0102061
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/cdb/ngi/ngi.html>)
Seq primer: M1 Reverse.
Location/Qualifiers
1. 416
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/note="Organ: brain; Vector: lambda B; Site_1: HindIII; Site_2: NotI"
/db_xref="ATCC (inhost):151218"
/db_xref="taxon:9606"
/clone_lib="Infant brain"
/sex="female"
/dev_stage="infant"
<1. >416

FEATURES

SOURCE

BASE COUNT

116 a 116 c 93 g 86 t 5 others

ORIGIN

Query Match

8.6%

Score 190.

DB 25.

Length 416.

Best Local Similarity 84.9%

Pred. No. 0.00e+00.

Matches 241.

Conservative 0.

Mismatches 41.

Indels 2.

Gaps 2.

Db

1

CCACTGCCACGCTTCTGCGAGAGAGGGGCTGAAGCCAACTCCAAAGATTAGC

60

0y

1870

CCACTGCG-ACATTTATTCAGAGGCAAGGGCTGAAGCCAACTCCAAAGATTAGC

1928

Db

61

ATGTCCTTCACAGAGCTACGACAAATATTCATCCAGGAGATTAACAAGGTATCAAACT

120

[illegible]

[illegible]

RESULT	9								
LOCUS	T03342	319 bp	mRNA	EST	14-FEB-1997				
DEFINITION	IB1289	infant brain,	Bento Soares	Homo sapiens	CDNA clone IB1289				
		3' end, mRNA sequence.							
ACCESSION	T03342								
NID	9314582								
KEYWORDS	EST.								
SOURCE	human.								

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT

1 (bases 1 to 319)
Khan,A.S., Wilcox,A.S., Polymeropoulos,M.H., Hopkins,J.A.,
Stevens,T.J., Robinson,M., Orpana,A.K. and Skreka,J.M.
Single pass sequencing and physical and genetic mapping of human
CDMS
Nature Genet. 2, 180-185 (1992)
94258200
On Jul 31, 1993 this sequence version replaced gi:275999.

Contact: Sikelela JM
 Department of Pharmacology
 University of Colorado Health Sciences Center
 Box C236, 4200 E. 9th Ave, Denver CO 80262-0236
 Tel: 3032708657
 Fax: 3032707097
 Email: njkik@eternity.uchsc.edu
 Seq primer: -21m13 Universal.
 Location/Qualifiers
 I. .319
 source

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/adb_host="E. coli DH5-alpha"
complement(<1..>319)
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<1..>319
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BASE COUNT      60 a      73 c      87 g      92 t      7 others
ORIGIN

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Query Match      8.3%  Score 183:  DB 23:  Length 319:
Best Local Similarity 80.6%:  Pred. No. 0.00e+00:
Matches 222;  Conservative 0;  Mismatches 56;  Indels 0;  Gaps 0

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RESULT	LOCUS	10
AA377675	225 bp	mRNA
EST99281	Synovial sarcoma	Homo sapiens CDNA 5' end, mRNA sequence.
AA377675		
NID	g2029994	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	

Vertebrata: Mammalia; Eutheria; Primates; Catarrhini; Hominoidea: Homo.

1 (pages 1 to 225)

Adams, M.D., Karlavag, A.R., Fletschmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kitzneag, E.P., Weinstein, K.G., Goecky, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, A.D., Earle-Hughes, J., Fife, L.D., Fitzgerald, D.M., Fitzhugh, W.M., Fitchman, E., Geoghegan, N.S., Glocker, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.

REFERENCE

AUTHORS

MORENO-PALANCUES, R.F., McDONALD, L.A., NGUYEN, D.T., PELLIGRINO, S.M., PHILLIPS, C.A., RYDER, S.E., SCOTT, J.L., SAUDEK, D.M., SHIPLEY, R., SMALL, K.V., SPRIGGS, T.A., UTTERBECK, T.R., WEIDMAN, J.F., LI, Y., BEDNARIK, D.P., CAO, L., CEPEDA, M.A., COLEMAN, T.A., COLLINS, E.J., DIMKO, D., FENG, D.-F., FERTLE, A., FISCHER, C., HASTINGS, G.A., HE, W.W., HU, J.S., GREENE, J.M., GRUBER, J., HUDSON, P., KIM, A.K., KOZAK, D.L., KUNTSCH, C., HUNGJUN, J., LI, H., MELISSNER, P.S., OLSEN, H., RAYMOND, L., WEI, Y.-F., WANG, J., XU, C., YU, G.-L., RUBEN, S.M., DILLON, P.J., FANNON, M.R., ROSEN, C.A., HASSETLINE, W.A., FIELDS, C., FRASER, C.M. and VENTER, J.C.

TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

JOURNAL Nature 377 (6547 Suppl.), 3-174 (1995)

MEDLINE 96026280

Contact: Kerlavage, AR
Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR <http://www.tigr.org/tdb/hg1/hg1.html>;
Index (<http://www.tigr.org/tdb/hg1/hg1.html>)
Seq primer: M13 Reverse
Location/Qualifiers
FEATURES
source
1..225

FEATURES	source	Location/Qualifiers
BASE COUNT	119 a 184 c 157 g 74 t	32 others
ORIGIN		
Query Match	5.7%	Score 149; DB 25; Length 225;
Best Local Similarity	85.4%	Pred. No. 1,62e+246;
Matches	187; Conservative	0; Mismatches 30; Indels 2; Gaps 2;
Db	3 TCCTGCTCTTCTTTCTTTCTAGACGAGACCCCTCGCTCTTTGGCCAGACCCCTCTCCCTGC 62	
Qy	691 TCTTCTCTCCCATACCTACCCAGACGAAACCTCCGCTCTTTGGCCAGACCCCTCTCCCTGC 750	
Db	63 AGGGCCCCGAGCTCCACGCGCTGGCGCCCCCAGAGTGAGCTGTGC -GGCCCAATAGACTGT 121	
Qy	751 AGGGCTCTGAGCTCCAGCGCTGGCGCCCCCAGAGTGAGCTGTGTGCGGCGCAATAGACTGT 810	
Db	122 GTGGCGCGCAATCCAACTGCAGCTCTGTGCACCGNACTGTGGCGGCAATGCTGTGGCAGGNC 181	
Qy	811 GTGGGCTGTGATCCCAATGCAAGCTCCGATGACGCGACACCTTGGCGGCAATGCTGTGGCAGGNC 870	
Db	182 GCGACGAAACACCATCTGTC -AACAGAGAGTTCACG 219	
Qy	871 GGGATCCCAATACCATCTGTCGCCAATAGAGAGTCCAGG 909	
RESULT	11	
LOCUS	FR0032477	566 bp DNA GSS 27-JUN-1998
DEFINITION	Fugu rubripes GSS sequence, clone 142F04d9, genomic survey	
ACCESSION	AL028845	
NID	93270959	
KEYWORDS	GSS: genome survey sequence.	
SOURCE	Fugu rubripes.	
ORGANISM	Fugu rubripes.	
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Perciformes; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.	
AUTHORS	Elgar, G., Clark, M., Smith, S., Meek, S., Warner, S., Umranta, Y., Williams, G. and Brenner, S.	
TITLE	Direct Submission	
JOURNAL	Submitted (09-JUN-1998) MRC Human Genome Mapping Project Resource Centre, Hinxton, Cambridge, CB10 1SB, UK. Email: biohelp@hmp.mrc.ac.uk	
COMMENT	Vector: Bluescript II KS	
	V_Type: phagemid	
	PRIMER: KS	
	DESCR: One pass dye-terminator sequencing of cosmid cloned genomic sequence.	
FEATURES		
source		
	1..366	
	/organism="Fugu rubripes"	
	/db_xref="taxon:31033"	
	/clone_1lb="cosmid 142F04"	
	/clone="142F04d9"	
BASE COUNT	119 a 184 c 157 g 74 t	32 others
ORIGIN		
Query Match	5.2%	Score 116; DB 27; Length 566;
Best Local Similarity	66.8%	Pred. No. 2,50e+176;
Matches	217; Conservative	0; Mismatches 107; Indels 1; Gaps 1;
Db	26 CACCAGCGGCTGAGACGCCGCNAGCCTGCMACATGACAGANNACCTGCGAGAGCTCGG 85	

OY	1145	CACACCAGCTGGATGCGGCCAAGGCCTGTCAACTGAATACAACTGCAGAAGCTTCG	1204
Db	86	CACGGGAGTACGTGTGCGCCTGCATCCAGCCCTCAGCCCGGTCCGGCCCCGTGNACGGGC	145
OY	1205	CTCCCTCT-TATAATCTCCATCTGCAACCGTGATCATCTCTCCACCGAACGCTGCAACCGCC	1263
Db	146	CCAAGTGCACAAGAAGCGCCNGANGAAGTCTTCGACACGGGGTCTCCCCCGCACTACACCCACG	205
OY	1264	GCAAATGTGCACAAGAGCTGTGGCGCAGTTCTTTGACCGGTGTGCCAGCAGATATACCTACG	1323
Db	206	AGCTGCTCTTTCTNACCCCTGCACCGACNCGNCTGTGCAGACGCGCGCGCCAGACCATCG	265
OY	1324	GCATGCTCTTTCTGCTCCTGTAGAGCACGAGCATGTGCTGACACGTTCGCCGCAACCATCC	1383
Db	266	TCCCGTCTCTGCTCTCTACNAGACNAGAGAAAGCCCACTGCTGCTGACTGCGCGCTCT	325
OY	1384	TGCCAGTGTGCTCTATGAGACAGAGAGAACCCCACTGCTGACTGCGCAGCTGT	1443
Db	326	GCAACGCCGACTACGTGTGCAAGTC	350
OY	1444	GTCGTACAGCACCTGTGCGGTC	1468
LOCUS	12	AA518362	631 bp mRNA EST 16-JUL-1997
DEFINITION	V110D02.1	Barnstead mouse myotubes MPLRB5 Mus musculus cDNA	
ACCESSION	903363 5,	AA518362	mRNA sequence.
NID	g2259047		
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
	Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;		
	Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Mur.		
REFERENCE	Murine; Mus.		
AUTHORS	1 (bases 1 to 631)		
	Marra,M., Hallier,L., Allen,M., Bowles,M., Dietrich,N., Im-		
	Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,		
	Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,J.,		
	Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and		
	Waterston,R.		
TITLE	The WashU-HMI Mouse EST Project		
JOURNAL	Unpublished (1996)		
COMMENT	Contact: Marra M/Mouse Est Project WashU-HMI Mouse Est Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@wustl.edu This clone is available royalty-free through LNL : contact the IMAGE Consortium (info@image.lnl.gov) for further information. Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 259. Location/Qualifiers 1..631 /organism="Mus musculus" /strain="C3H" /note="Vector: pUT73D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTATCAATCTGTAAGTGGAGAGCGCGCCGCTTTTTTTTTTTTTTTTTTTT; 3']; double-stranded cDNA was ligated to Eco RI adaptors (AATTGGATCTTG), digested with Not I and cloned into the Not I and Eco RI sites of the modified pUT73 vector. Library constructed by Bob Barnstead. The C2C12 cell line (available from ATCC, catalog # CRL-1772) differentiates rapidly, forming contractile myotubes and producing characteristic muscle proteins." /db_xref="taxon:10090"		

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strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCATCTGAGTGGAGCGGCGCCGCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRT3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M. Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBHL19W."

/db_xref="taxon:9606"
/clone="344593"
/clone_lib="Soares fetal heart NBHL19W"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
BASE COUNT 112 a 145 c 130 g 90 t 1 others
ORIGIN

Query Match 10.1% Score 426: DB 21: Length 478:
Best Local Similarity 98.1%: Pred. No. 0.00e+00:
Matches 464: Conservative 0: Mismatches 3: Indels 6: Gaps 6:

Db 1 TGACACCTAATCTATGTGACTCCAGCCCATCTGCATCGTGTGTCCTCCCTGCTGACACT 60
Oy 2500 TGACACCTAATCTATGTGACTCCAGCCCATCTGCATCGTGTGTCCTCCCTGCTGACACT 2559
Db 61 GTCCGCGCAGCGGGGAACTGAGAGAGAGTGTGAAATTTCTCTAGGGACTTCACCGAGA 120
Oy 2560 GTCCGCGCAGCGGGGAACTGAGAGAGAGTGTGAAATTTCTCTAGGGACTTCACCGAGA 2619
Db 121 ACCCATGCTCCGGAAGCCATCCAGGCTTTGN--ACGGCAGGAGCGTGAACGTGTCC 179
Oy 2620 ACCCATGCTCCGGAAGCCATCCAGGCTTTGN--ACGGCAGGAGCGTGAACGTGTGTCC 2679
Db 180 CAAAAGGCCCTCTGTTCCAGGCGCCAGGCC--TCGGGTGAGAGAAGCGCTTTCTTTC 238
Oy 2680 CAAAAGGCCCTCTGTTCCAGGCGCCAGGCCCTCGGGTGAAGAGCGCTTTCTTTC 2739
Db 239 CAGATGACCTCAGTACAGTACAGCTTGGGAGCAGTGTATCATCCACCTGCACAGTGTG 298
Oy 2740 CAGATGACCTCAGTACAGTACAGCTTGGGAGCAGTGTATCATCCACCTGCACAGTGTG 2799
Db 299 TCACGAGCAGGCGCTGAGGCGCAACACCTCAAGAGTAAAGTATGATGCTTCACAGAGC 358
Oy 2800 TCACGAGCAGGCGCTGAGGCGCAACACCTCAAGAGTAAAGTATGATGCTTCACAGAGC 2859
Db 359 TCACGAGCAAAATATCATCCAGGCGAATACAGAGTGAATCAAACTTAACAGGCCCGAG 418
Oy 2860 TCAC--GACAAATATCATCCAGGCGAATACAGAGTGAATCAAACTTAACAGGCCCGAG 2917
Db 419 CAGAGCAGAGCGCTGCGCTTGTGACCGTGTGTCTGTCTGTATCTGTA 471
Oy 2918 CAGAGCAGAGCGCTGCGCT--GACCTT--GACCGTGTGTCTGTCTGTATCTGTA 2968

RESULT 2
LOCUS AA747512 476 bp mRNA EST 18-FEB-1998
DEFINITION nx77d04.s1 NCI-CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1268263, mRNA
sequence.
ACCESSION AA747512
NID 92787470
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Homo.

REFERENCE
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Lee Helman, M.D., Michael R. Fennell, Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information found through the I.M.A.G.E. Consortium/LNL at: www-bio.11nl.gov/dbtrp/image/image.html

Insert Length: 361 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence step: 401.
Location/Qualifiers

FEATURES

source

1. 476

/organism="Homo sapiens"

/note="Vector: PAMP10; mRNA made from Ewing's sarcoma"

CDNA made by oligo-dT priming. Non-directional.

Size-selected on agarose gel, average insert size:

Reference: Krizman et al. (1996) Cancer Research

56:5380-5383.

/db_xref="taxon:9606"

/clone="IMAGE:1268263"

/clone_lib="NCI-CGAP_Ew1"

/tissue_type="Ewing's sarcoma"

/lab_host="DH10B"

BASE COUNT 131 a 104 c 119 g 121 t 1 others
ORIGIN

Query Match 9.5% Score 403: DB 13: Length 476:
Best Local Similarity 97.3%: Pred. No. 0.00e+00:
Matches 429: Conservative 0: Mismatches 9: Indels 3: Gaps 3:

Db 37 ACGTTTATGAGAGCTTGTGTTAAGCTTGATGCGATCAGAGAGCCGCCACAGGCCAG 96
Cp 4229 ACGTTTATGAGAGCTTGTGTTAAGCTTGATGCGATCAGAGAGCCGCCACAGGCCAG 4170
Db 97 CCAGGCTGACTGGGCGAGGCGCAGTGTCTTTTCCCATTAATAGACAC 156
Cp 4169 CCAGGCTGACTGGGCGAGGCGCAGTGTCTTTTCCCATTAATAGACAC 4110
Db 157 AGATTAAAAAATAAATTACATTAATATATATTTTCCCTATGTTGGGATATT 216
Cp 4109 AGATTAAAAAATAAATTACATTAATATATATTTTCCCTATGTTGGGATATT 4050
Db 217 TCATAGTTTGTGCTTAAAAAAGAAAGGAAAGGAAACACATATATATAT 276
Cp 4049 TCATAGTTTGTGCTTAAAAAAGGAAAGGAAAGGAAACACATATATATAT 3990
Db 277 GGATGTAT 336
Cp 3989 GGATGTAT 3930
Db 337 CGCTAGGAATGAGAAAGAGCGCGCAAGCGCGAGAGGAGAGAGACAGAGA 396
Cp 3929 CGCTAGGAATGAGAAAGAGAGCGCG--AAAG--GAGGAGAGAGAGAGAGAGAGA 3872
Db 397 AAGCTTGAGGCGCA--GGTCTCGACAGACACACCGGCTGTGTCTTCCCTCCCT 455
Cp 3871 AAGCTTGAGGCGCAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3812
Db 456 CCCCAAGGAGGCGCTGCCAA 476
Cp 3811 CCCCAAGGAGGCGCTGCCAA 3791

RESULT 3
LOCUS W73633 433 bp mRNA EST 16-OCT-1998
DEFINITION z053h01.s1 Soares fetal heart NBHL19W Homo sapiens cDNA clone
344593 3', mRNA sequence.

ACCESSION	N73633
NID	G1383767
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homidae; 1 (bases 1 to 433)
AUTHORS	Hillier,L., Clark,N., Dubaque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rikkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.
TITLE	The Mashu-Merck EST Project
JOURNAL	Unpublished (1995)
COMMENT	Contact: Wilson RK Mashu-Merck EST project Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.wustl.edu This clone is available royalty-free through LINT ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 650 Std Error: 0.00 Seq primer: mob.REGA+ET High quality sequence stop: 343. Location/Qualifiers 1..433 /organism="Homo sapiens" /note="Organ: heart; Vector: pTR73D (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer TGTTACAATCTGAGTAGTGAGCGGCCGCATCTTTTTTTTTTTT 3'1, IGTTACCAATCTGAGTAGTGAGCGGCCGCATCTTTTTTTTTTTT 3'1, double-stranded cDNA was selected, ligated to Eco I adapters (Pharmacia), digested with Not I and cloned in the Not I and Eco RI sites of a modified pTR73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Felima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBH19W." NBH19W." /db_xref="taxon:9606" /clone="344593" /clone_lib="Soares fetal heart NBH19W" /sex="unknown" /dev_stage="19 weeks" /lab_host="DH10B (ampicillin resistant)" complement(<1..>433) BASE COUNT 72 a 109 c 132 g 120 t ORIGIN Query Match 8.8%; Score 372; DB 21; Length 433; Best Local Similarity 97.9%; Pred.No. 0.00e+00; Matches 411; Conservative 0; Mismatches 3; Indels 6; Gaps 5
Db	1 GCACGGTGTGTGTGTGTGTGTGTGTTCATTTCGTGACAGCCGGCTTCTGTCTCCG 60
Cp	3077 GCACGGTGTGTGTGTGTGTGTGTGTTCATTTCGTGACAGCCGGCTTCTGTCTCCG 3018
Db	61 TA-CTTTAAATAATTTCTGACTCGGTCCACAGACCCTACAGAAGCCTTTCCAGCATAG 119
Cp	3017 TAGCTTTAAAATCTTTGTGACTCGGTCCACAGACCCTACAGAAGCCTTTCCAGCATAG 2958
Db	120 GACACAGACAGCAGGTGCAAGGACGCGACGGTCTGGCTCTGGTGGGCGCTGAGTTAGTTT 179
Cp	2957 GACAGACAGCAGCGTCAAGGACGCGACGGTCTGGCTCTGGTGGGCGCTGAGTTAGTTT 2898
Db	180 GATCACCTTGTAACCCCCTGGAGATATTTTGCTGTAGCTCTGTGAGACACATGCTTAA 239
Cp	2897 GATCACCTTGTAACCCCCTGGAGATATTTTGCTGTAGCTCTGTGAGACACATGCTTAA 2838

Db	240	CTCTTTGGAGTGTGGCCTTCACGCCCCCTCTCTCGACACAGACTGCAGTGATGAC	299
Cp	2837	CTCTTTGGAGTGTGGCCTTCACGCCCCCTCTCTCGACACAGACTGCAGTGATGAC	2778
Db	300	ACTGGGTCCTCCAACTGCTGACTCATGAGTCATCTGCAAGAAGAGCGCTTTCACA	359
Cp	2777	ACTGG-TGCCAACCTGTAAGTCACTGAAGTCATCTGCAAGAAGAGCGCTTTCACA	2719
Db	360	CCCAGAGGGGCGCTGGGCTGGCTGGACAGAGGGGCGCTTTTGGGGCACACGTTACGTT	419
Cp	2718	CCCAGAGGGGCGCTGGG-TGGCGCTGGACAGAGAGG-CCTTTT--GGGACACGTTACGTT	2663
RESULT	4		
LOCUS	AA350341	416 bp	mRNA
DEFINITION	EST57915	Infant brain Homo sapiens	cDNA 5' end, mRNA sequence.
ACCESSION	AA350341		
NID	G2002900		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Carnivora; Hominoidea.		
AUTHORS	1 (bases 1 to 416) Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Feldner,R.A., Bilt,C.J., Lee,N.H., Kirnes,E.F., Weinstock,K.G., Cline,J.C., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Nottingham,Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,E., Fitzgerald,L.M., Fitzhugh,W.M., Friedman,J.L., Gish,W.B., Glodek,A., Gnehm,C.L., Hanna,M.C., Heblum,E., Hinkley,S., Kelley,J.M., Kelley,J.C., Liu,I.-I., Marrairos,S.H., McCreery,Moreno-Palmer,R.F., McDonald,L.A., Nguyen,D.T., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Small,K.V., Spriggs,T.A., Utechtack,T.R., Weidman,J.L., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Coulter,Dmke,D., Fang,D.-F., Ferris,A., Fischer,C., Haselinger,H.W.M., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kozak,D.L., Kunsch,C., HungJun,J., Li,H., Meltsner,B., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fraser,C.M. and Venter,J.C. Initial assessment of human gene diversity and expression based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl.), 3-174 (1995)		
JOURNAL MEDLINE COMMENT	Other-ESTs: EST57914 TRC102061 Contact: Kerlavage, AR Bioinformatics The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056 Fax: 3018699423 Email: arkerlav@tigr.org For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Index (http://www.tigr.org/cdb/hgl/hgl.html) Seq primer: M13 Reverse.		
FEATURES SOURCE	Location/Qualifiers 1..416 /organism="Homo sapiens" /note="Organ: brain; Vector: lafmid BA; Site_1: HindIII; Site_2: NotI" /db_xref="ATCC (inhost):J51218" /db_xref="taxon:9606" /clone_lib="Infant brain" /sex="female" /dev_stage="Infant" <1..>416		
BASE COUNT	116 a 116 c 93 g 86 t 5 others		
ORIGIN			

RESULT	8	AA349976	350 bp	MRNA	EST	21-APR-1997
LOCUS		AA349976	350 bp	MRNA	EST	21-APR-1997
DEFINITION		EST55965	Infant brain	Homo sapiens	cdNA 5' end, mRNA sequence.	
ACCESSION		AA349976				
NID		g2002296				
KEYWORDS		EST.				
SOURCE		human.				
ORGANISM		Homo sapiens				
REFERENCE		1. (bases 1 to 350)				
AUTHORS		Adams, M.D., Kerlavage, A.R., Fields, C. and Venter, J.C.				
TITLE		3,400 expressed sequence tags identify diversity of transcripts from human brain				
JOURNAL		Nature Genet. 4, 256-267 (1993)				
MEDLINE		93364420				
COMMENT		Other ESTs: THC102061 Contact: Kerlavage, AR Bioinformatics The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056 Fax: 3018699423 Email: arkerlav@tigr.org For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html) Seq primer: M13 Reverse. Location/Qualifiers 1..350 /organism="Homo sapiens" /note="Organ: brain; Vector: lambdafmd BA; Site_1: HindIII; Site_2: NotI" /db_xref="ATCC (inhost):150854" /db_xref="taxon:9606" /clone_lib="infant brain" /sex="female" /dev_stage="infant" <1..350 80 a 105 c 93 g 62 t 10 others				
BASE COUNT		80 a 105 c 93 g 62 t 10 others				
ORIGIN		MRNA				
		Query Match	7.8%; Score 328; DB 25; Length 350;			
		Best Local Similarity 96.0%; Pred. No. 0.00e+00;				
		Matches 337; Conservative	0; Mismatches 13; Indels 1; Gaps 1;			
Db	1	CAGCCCCACATGCGATCGTGTGTCCTCCCTGGTGCAGCTGTCTGTGNNAGCGGGAACATGGA	60			
OY	2522	CAGCCCCACATGCGATCGTGTGTCCTCCCTGGTGCAGCTGTCTGTGNNAGCGGGAACATGGA	2581			
Db	61	GGAGAGAGTGNAGAGTTCTCTCAGGAGACTCACCGAGAACCCATGCTCCGGAAGCGCAT	120			
OY	2582	GGAGAGAGTGNAGAGTTCTCTCAGGAGACTCACCGAGAACCCATGCTCCGGAAGCGCAT	2641			
Db	121	CCAGGCGCTTTGGCAACGCGCACGAGCGTNAACGTNTCCCAAAAGGCGCCCTGTTCCAGGC	180			
OY	2642	CCAGGCGCTTTGGCAACGCGCACGAGCGTNAACGTNTCCCAAAAGGCGCCCTGTTCCAGGC	2701			
Db	181	CACCCAGGCGCCCTGGGNTGGAGAGACGCGCTTTCTTTCACGATGAGTACTCATGTTNACAGTAC	240			
OY	2702	CACCCAGGCGCCCTGGGNTGGAGAGACGCGCTTTCTTTCACGATGAGTACTCATGTTNACAGTAC	2761			
Db	241	CAGCTTGGGAGACAGTGTGCATCACACCTGCAGCTTTNTCCAGAGAGCAGGGGCTGAAGGC	300			
OY	2762	CAGCTTGGGAGACAGTGTGCATCACACCTGCAGCTTTNTCCAGAGAGCAGGGGCTGAAGGC	2821			
Db	301	AACAACTCCAAAGAGTTAAGCATGTGTTCTTTCAGAGCTCACGGCAATAT	350			
OY	2822	CAACAACCTCCAAAGAGTTAAGCATGTGTTCTTTCAGAGCTCACGGCAATAT	2872			

LOCUS	H05619	418 bp	mRNA	EST	21-JUN-1995
DEFINITION	Y170a10.s1 Homo sapiens cDNA clone 43207 3'.				
ACCESSION	H05619				
NID	9869171				
KEYWORDS	EST.				
SOURCE	human clone-43207 library=Soares infant brain IN1B vector=lambda HA host=DH10B (ampicillin resistant) primer=Promega -21m3 RstE1-NciI I RstE2-Hind III whole brain from a 73 days post natal female. 1st strand cDNA was primed with a Not I - oligo(dt) primer (5' AACTGGAAGAAATTCGGCGCCGACGAGAAATTTTCTTTTCTTTT 3'); double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the lambdafmd BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Felima Bonaldo.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryote; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonmata; Tetrápoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 418)				
AUTHORS	Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucab,T., Le,M., Lennon,G., Marra,M., Parsons,T., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Woldmann,P. and Wilson,R.				
TITLE	The Washu-Merck EST Project				
JOURNAL	Unpublished (1995)				
COMMENT	GDB: G00-415-748 Contact: Wilson RK Washu-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu High quality sequence stops: 364 Source: IMAGE Consortium, LNLN. This clone is available royalty-free through LNLN : contact: IMAGE Consortium (info@image.lnl.gov) for further information Location/Qualifiers 1. 418 /organism="Homo sapiens" /clone="43207"				
BASE COUNT	73 a 94 c 116 g 127 t 8 others				
ORIGIN					
Query Match	7.4%; Score 312; DB 16; Length 418;				
Best Local Similarity	95.1%; Pred.No. 0.00e+00;				
Matches	388; Conservative 0; Mismatches 8; Indels 12; Gaps				
Db	11 TGGGAAAAACATTTTTTTTTTTTGGCAAGGTGCTGTCTGTCTGTCTGTCTTCATTTCC				
Cp	3099 TGGGAAAAACATTTTTTTTTTTTGGCAAGGTGCTGTCTGTCTGTCTGTCTTCATTTCT				
Db	71 CAGGCGGCTGTTCTTGTCTGCGGTANTTTCAAATCTTTGACTCGGTTCCCAACACCT				
Cp	3039 CAGGCGGCTGTTCTTGTCTGCGGTANTTTCAAATCTTTGACTCGGTTCCCAACACCT				
Db	131 ACAAGGCGCTGTTTTCAGCATCAGACAGACAGACAGCGGTCAAGGACCGCGCTCAGCT				
Cp	2979 ACAAGGCGCATTTTCAGCATCAGACAGACAGACAGCGGTCAAGGACCGCGCTCAGCT				
Db	191 TCGTGGGGCCGTAATTAGTTTGATTCACCTGTTTACCTCCCTGGGATGATATTTCGATCA				
Cp	2919 TCGTGGGGCCGTAATTAGTTTGATTCACCTGTTTACCTCCCTGGGATGATATTTCGCA				
Db	251 GCTGTGGAACACATGTTTAACTCTTTGGATTTTGGCTTACGAGCCCTGCTCTGGG				
Cp	2859 GCTGTGGAACACATGTTTAACTCTTTGGATTTTGGCTTACGAGCCCTGCTCTGGG				
Db	311 ACAGAACGTGTCAGAGTGGGTGATGACACTGGGNCCTCAAGGCTGGTACTGTCACTGAGG				

CP	2800	ACAGA-CGTGAGG-TGG-TGATGACACATCG-TCCCAAG-CTGG-TACTGTCACTAGAG	2747
Db	371	GTGATCTGGNCAAGNAGNCCTTTTCTCCACCCGAGGGCCGGG	418
CP	2746	-TCATCTGG-CAAG-AGG-CGCTT-CTCCACCCGAGGGCCG	2704
RESULT	10	HSC2YA051	317 bp RNA EST 21-SEP-1995
LOCUS		H. sapiens partial cDNA sequence; clone C-2ya05, mRNA sequence.	
DEFINITION		F08597	
ACCESSION		9677164	
NID		EST: partial cDNA sequence; transcribed sequence fragment.	
KEYWORDS		human.	
SOURCE		Human sapiens	
ORGANISM		Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	
REFERENCE		1 (bases 1 to 317)	
AUTHORS		Genexpress.	
TITLE		Direct Submission	
JOURNAL		Submitted (11-JAN-1995) Genethon, B.P. 60, 91002 Evry Cedex France and Genetique Moleculaire et Biologie du developpement, CNRS UPR420 B.P. 8, 94801 Villejuif Cedex France E-mail: genexpress@genethon.fr	
REFERENCE		2 (bases 1 to 317)	
AUTHORS		Genexpress.	
TITLE		The Genexpress cDNA program	
JOURNAL		Unpublished	
REFERENCE		3 (bases 1 to 317)	
AUTHORS		Auffray,C., Behar,G., Bols,F., Boucher,C., da Silva,C., Devignes,M.D., Duprat,S., Houligatte,R., Juneau,M.N., Lamy,B., Lorenzo F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouillot,Y., Sebastien,F.,Kbakchich,C. and Tessier,A.	
TITLE		IMAGE: molecular integration of the analysis of the human genome and its expression	
JOURNAL		C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)	
MEDLINE		95277534	
COMMENT		Cloning method: total mRNA was oligo-(dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the lambdaID BA vector.	
FEATURES		Sequencing method: single read, full automatic;	
SOURCE		Primer: M13-reverse	
		cDNA sequence colinear to mRNA	
		Stretch removed: nothing	
		Normalization method: Bento Soares, P.N.A.S. 91:9228-9232(1994);	
		Genexpress library_id: C;	
		Genexpress sequence_id: Y1C-2ya05.	
		Location/Qualifiers	
		1. 317	
		/organism="Homo sapiens"	
		/isolate="muscular atrophy patient"	
		/db_xref="taxon:9606"	
		/clone_lib="normalized infant brain cDNA from B.Souares, psychiatry Dept. Columbia University USA"	
		/sex="female"	
		/tissue_type="total brain"	
		/dev_stage="3 months old"	
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Query Match	7.3%	Score 307;	DB 20; Length 317;
Best Local Similarity	96.8%	Pred. No. 0.00e+00;	
Matches 307; Conservative	0;	Mismatches 10;	Indels 0; Gaps 0;
Db	1	GGCTGGGGGCGACGCCAGAGGGGCTTGAGAGCTGAGCTGCGTGGNAGCCCTTNGG	60
Oy	3628	GGCTGGGGGCGACGCCAGAGGGGCTTGAGAGCTGAGCTGCGTGGGAGACCCCTTGGG	3687
Db	61	CGAGGCAATTAACCTTGGGACACAGCTTCTTNTCGGTGGAGAAATTTNAAGTCAGAG	120
Oy	3688	CGAGGCAATTAACCTTGGGACACAGCTTCTTCTCGGTGGAGAAATTTTGAAGTCAGAG	3747
Db	121	AGAAAGGCTCTTTTGTGGCTTTCTTCTTCTGCTGCTGAGGCTCCTTTGGCAGGCTCCCTTT	180

OY	3748	AGAAACGGTCTTTTGTGCGCTTCTTGCTTCCTGGGTCCTTTGGAGCGCTCCCTTT	3807
Dd	181	GGGAGAGAGGAGGAGAGACACACAGCCGGGTGTTGTCTGCAGCAGCGTGGGCCCTCA	240
OY	3808	GGGAGAGAGGAGGAGAGACACAGCCGGGTGTGTCTGCAGCAGCAGCGTGGGCCCTCAA	3867
Dd	241	GCTTCCTGCGTNTTCTCCCTCCCTCCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTA	300
OY	3868	GCTTCCTGCGTNTTCTTCCTCCCTCCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTA	3927
Dd	301	CCTAGCTCAACTGTATG 317	
OY	3928	CCTAGCTCAACTGTATG 3944	
RESULT	11	H12981	521 bp mRNA EST 27-JUN-1995
LOCUS	DEFINITION	V170a10.r1 Homo sapiens cDNA clone 43207 5'	
ACCESSION		H12981	
NID		9877801	
KEYWORDS		EST.	
SOURCE		human clone=43207 library=Soares infant brain INIB vector=Lafmid BA host=PH10E (ampicillin resistant) primer=M3RPI RstleI-Not I Rstle2-Hind III Whole brain from a 73 days post natal female. 1st strand cDNA was primed with a Not I - oligo(dT) primer 15' AACTGAGAAGATCCGCGCCGACAGAAATTTTTTTTTTTT 3'; double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lafmid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryote; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chondrata; Tetrapoda; Amniota; Mammalia; Theria;	
AUTHORS		Eubelia; Archonta; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 521)	
TITLE		Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Holtzman,M., Kucaba,T., Le,M., Lennon,G., Marre,M., Parsons,D., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevisakis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.	
JOURNAL		The Washu-Merck EST Project	
COMMENT		Unpublished (1995)	
FEATURES		GDB: G00-415-748 Contact: Wilson RK Washu-Merck EST project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63107 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.wustl.edu High quality sequence stops: 278 Source: IMAGE Consortium, LNLN. This clone is available royalty-free through LNLN, contact: IMAGE Consortium (info@image.lnl.gov) for further information.	
BASE COUNT		95 a 154 c 144 g 119 t 9 others	
ORIGIN		1..521 /organism="Homo sapiens" /clone="43207"	
Query Match		7.3%; Score 307; DB 16; Length 521;	
Best Local Similarity		93.6%; Pred. No. 0.00e+00;	
Matches		396; Conservative 0; Mismatches 14; Indels 13; Gaps	
Dd	1	CAACCATTCGCTGGGATGCTGCCAAGGCTCCACAAGTAAGACACTGCAAGAAGCTTC	
OY	2060	CAACCATTGCTGCG-ATGCTGCCAAGGCTCCACAAGTAAGACACTGCAAGAAGCTTC	

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu

High quality sequence stops: 312
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Location/Qualifiers
1. .359
/organism="Homo sapiens"
/clone="123205"

FEATURES

source

BASE COUNT 74 a 92 c 79 g 111 t 3 others
ORIGIN

Query Match 6.7%: Score 285; DB 5; Length 359;
Best Local Similarity 96.6%: Pred. No. 0.00e+00;
Matches 313; Conservative 0; Mismatches 7; Indels 4; Gaps 3;

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Oy 3729 AGAATTTTGAAGTCAGAGAGAACGCTCTTGTGCTCTTGTGCTCTGTC 3788
Db 61 CTTGGCAGGCTCTCCCTTTGGAGAGAGAGAGACACAGCCGGGTGTGTC 120
   |||||||
Oy 3789 CTTGGCAGGCTCTCCCTTTGGAGAGAGAGAGAGACACAGCCGGGTGTGTC 3848
Db 121 CAGCACCGTGGGCTCTCAAGCTTCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 180
   |||||||
Oy 3849 CAGCACCGTGGGCTCTCAAGCTTCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 3908
Db 181 TCTTCTCTTTNCNAGSAGTACGTACGTATGTATACACCGGGCTCTCTCTCT 240
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Oy 3909 TCTTCTCTTTNCNAGSAGTACGTACGTATGTATACACCGGGCTCTCTCTCT 3967
Db 241 ACATATATGTATATACATCATCATATATATATATATATATATATATATATAT 300
   |||||||
Oy 3968 ACATATATGTATATACATCATCATATATATATATATATATATATATATAT 4025
Db 301 TTTTAAAGGCAACAAACTATGG 324
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Oy 4026 TTTTAAAG-CAACAAACTATGG 4048
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Search completed: Thu Mar 11 22:08:09 1999
Job time : 13946 secs.

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OY 3363 GGACACACAGCTGTTCCCAAGCTGCCACTCTGGGAGCCCGTGGGGCTGGCAGAG 3422

Db 1861 ggcacgctcagcggcggcagcgggctg 1888

OY 3423 GGCATCGGTACGCGGGCAGCGGGGCTG 3450

RESULT 2

ID T84979 standard; DNA: 453 BP.

AC T84979;

DT 27-APR-1998 (first entry)

DE Human EST-derived sequence y170a10.r1.

KW Glial cell derived neurotrophic factor receptor alpha; GDNFR alpha; GDNF; human; kidney disease; glomerulonephritis; therapy;

KM expressed sequence tag; EST: ss.

OS Homo sapiens

PN M09733912-A2.

PD 18-SEP-1997.

PF 13-MAR-1997; U04363.

PR 14-MAR-1996; US-618236.

PA (GETH) GENENTECH INC.

PI Klein RD, Moore MW, Rosenthal A, Ryan AM;

DR WPI: 97-470819/43.

PT Isolated glial cell derived neurotrophic factor receptor alpha -

PT useful to develop products to diagnose and treat associated

PT disorders, particularly enteric nervous system or kidney disorders

PS Example 1; Page 61; 100pp; English.

CC This DNA sequence comprises a human EST-derived sequence designated

CC y170a10.r1. It can be used to identify glial cell derived

CC neurotrophic factor receptor (GDNFR) sequences, including human

CC variants. Also suitable as probes for GDNFR sequences are another

CC human EST-derived sequence designated yeb3h05.r1 (see T84978), and

CC fragments of these EST-derived sequences (see T84980-81) or

CC proteins encoded by them. The invention relates to novel uses of

CC GDNF and its receptor. In particular, it relates to native rat

CC (GDNFR alpha (see W27327), its variants and soluble derivatives

CC (extracellular domain), chimeric GDNFR alpha and antibodies which

CC bind to the GDNFR alpha, including agonist and neutralizing

CC antibodies, as well as various uses for these molecules. It also

CC relates to assay systems for detecting ligands to GDNFR alpha,

CC systems for studying the physiological role of GDNF, diagnostic

CC techniques for identifying GDNF-related conditions, methods for

CC identifying molecules homologous to GDNFR alpha, and claimed

CC methods for the treatment of GDNF-related and GDNFR alpha-related

CC conditions, particularly kidney disease associated with

CC glomerulonephritis and enteric nervous system related disorders.

CC Transgenic and knockout animals are also claimed.

SQ Sequence 453 BP: 86 A; 152 C; 121 G; 91 T;

Query Match 8.5%; Score 359; DB 37; Length 453;

Best Local Similarity 95.6%; Pred. No. 3,82e-219;

Matches 433; Conservative 0; Mismatches 9; Indels 11; Gaps 11;

Db 1 gcaacccatctcgcgatgctgcgaagcgcgcgaacctgaatgaactgaagaagctgc 60

OY 2059 GCAACCTTCTGCTGATGCTGCCAAGGCTGCAACCTGATGACAACTGCAAGAAGCTGC 2118

Db 61 gctctctctacatctcattcgaacccgcgaatctgcaccacgagcgctgaacgcgc 120

OY 2119 GCTCTCTCTACATCTCCATCTGCACCGGATCTCGCCACCGACGCTGCAACGGCC 2178

Db 121 gcaagtgcccaagggcgcctgcgcgaftcttgacacggcgggcgccaggaataaccacac 180

OY 2179 GCAAGTGCCCAAGGCGCCCTGCGCAGTCTTGACCGGGTGCCAGGGAATTAACCTTACC 2238

Db 181 gcatgctctctcctcctgcgaagaacaggcgtgcgctgagcgcgcggaacacacacac 240

OY 2239 GCATGCTCTTCTGCTCTGCGCAGACGCGTGCTGAGCGCGCGCGGCAACCTACC 2298

Db 241 tgcacagctcctccatagagacaaggaagaccacactcctggaactcgtgagcgtgt 300

OY 2299 TGCCCACTCTCTCTATGAGAGACAAGAACCCCAACTGCTGAGACTCGTGCGCTGT 2358

Db 301 ggcagctgaccacactgtgtgcctccggcctngccagcttccattccacattgtctcag 360

OY 2359 GCCGAGCTACACACCTGTCTCGCTCCGCGCTGGCGACTT-CCATGCCAATT-GT-CCAG 2415

Db 361 ccttccctacagaaggggtaccagaagcctgccttngcggaacattaccagggcgtgtctg 420

OY 2416 CCT-CCTACCAAGACGG-TCACCAAG-CTGCCCT-GCGGACAATT-ACCAGG-CGTGTCT-G 2468

Db 421 ggccttctatgttgatgatgttggtttgacct 453

OY 2469 GCGCTTT-ATGCTGCATGATTGGGTTTGACAT 2500

RESULT 3

ID T84978 standard; DNA: 351 BP.

AC T84978;

DT 27-APR-1998 (first entry)

DE Human EST-derived sequence yeb3h05.r1.

KW Glial cell derived neurotrophic factor receptor alpha; GDNFR alpha; GDNF; human; kidney disease; glomerulonephritis; therapy;

KM expressed sequence tag; ss.

OS Homo sapiens

PN M09733912-A2.

PD 18-SEP-1997.

PF 13-MAR-1997; U04363.

PR 14-MAR-1996; US-618236.

PA (GETH) GENENTECH INC.

PI Klein RD, Moore MW, Rosenthal A, Ryan AM;

DR WPI: 97-470819/43.

PT Isolated glial cell derived neurotrophic factor receptor alpha -

PT useful to develop products to diagnose and treat associated

PT disorders, particularly enteric nervous system or kidney disorders

PS Example 1; Page 61; 100pp; English.

CC This DNA sequence comprises a human EST-derived sequence designated

CC yeb3h05.r1. It can be used to identify glial cell derived

CC neurotrophic factor receptor (GDNFR) sequences, including human

CC variants. Also suitable as probes for GDNFR sequences are another

CC human EST-derived sequence designated y170a10.r1 (see T84979), and

CC fragments of these EST-derived sequences (see T84980-81) or

CC proteins encoded by them. The invention relates to novel uses of

CC GDNF and its receptor. In particular, it relates to native rat

CC (GDNFR alpha (see W27327), its variants and soluble derivatives

CC (extracellular domain), chimeric GDNFR alpha and antibodies which

CC bind to the GDNFR alpha, including agonist and neutralizing

CC antibodies, as well as various uses for these molecules. It also

CC relates to assay systems for detecting ligands to GDNFR alpha,

CC systems for studying the physiological role of GDNF, diagnostic

CC techniques for identifying GDNF-related conditions, methods for

CC identifying molecules homologous to GDNFR alpha, and claimed

CC methods for the treatment of GDNF-related and GDNFR alpha-related

CC conditions, particularly kidney disease associated with

CC glomerulonephritis and enteric nervous system related disorders.

CC Transgenic and knockout animals are also claimed.

SQ Sequence 351 BP: 77 A; 117 C; 96 G; 57 T;

Query Match 7.0%; Score 295; DB 37; Length 351;

Best Local Similarity 96.5%; Pred. No. 4.75e-175;

Matches 302; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Db 39 gccaagagacaacatgctgtagatctgcgaagcctgcaactgaatgaacacgcaag 98

OY 2052 GCCAAGAGCAACATTGCTGTGATGCTGCAAGGCGCTGCAACCTGATGACAACTGCAAG 2111

Db 99 aagctgcctctctacatctcattcgaacccgcgaatctgcgccacgagcgcttc 158

OY 2112 AAGCTCGCTCTCTCTCACTCTCAATCTGCACCGGAGATCTCCGCCACGAGCGCTCC 2171

Db 159 aacgcgcgaagtgcacaagcgcctgcgcgaattcttcgacgggtgcccagcagatc 218

OY 2172 AACCGCGCGAAGTGGCCACAAGGCGCTGCGCCAGTCTTGACCGGGGTGCCAGCAGTAC 2231

KW infection; meningitis; myelopathy; Creutzfeldt-jakob disease;
 KW cranial nerve injury; spinal cord injury; Down's syndrome;
 KW cerebral palsy; Lyme disease; muscular dystrophy;
 KW myasthenia gravis; tumour; therapy; ds.
 OS Rattus sp.
 FH key Location/Qualifiers
 FT CDS 257..1663
 FT sig_peptide 257..328
 FT mat_peptide 329..1660
 FT /tag= b
 FT /tag= c
 PD WO9744356-A2.
 PD 27-NOV-1997.
 PF 07-MAY-1997: U07726.
 PR 10-APR-1997: US-017427.
 PR 08-MAY-1996: US-017427.
 PR 07-JUN-1996: US-019300.
 PR 16-JUL-1996: US-021859.
 PA (BioJ) BIOGEN INC.
 PI Cate RL, Hession C, Sanicola-Nedel M;
 DR WPI: 98-018431/02.
 PT P-PSNB: W37457.
 PT New nucleic acid encoding ret receptor ligands and related proteins
 PT -vectors, transformed cells and antibodies, used for promoting cell
 PT growth and improving survival of injured cells, especially renal or
 PT nerve cells
 PS Claim 1: Page 46-49; 113pp; English.
 CC This sequence comprises rat retL1 cDNA (deposited as ATCC 98047)
 CC that codes for the Ret ligand RetL1 (see W37457), a key component
 CC of the Ret signalling pathway. It consists of the insert of clone
 CC #230-5A-86-17 that was isolated from a rat embryonic kidney cDNA
 CC expression library using a rat Ret/IgG fusion protein. The
 CC isolated cDNA was used as a probe to identify human retL1 cDNA
 CC (see V00246-47). retL2 and retL3 cDNAs have also been identified
 CC (see V00248-51). Vectors containing retL1 DNA and prokaryotic or
 CC eukaryotic host cells transformed or transfected with these vectors
 CC are claimed, as well as a method for production of RetL1, its
 CC soluble variants and fusion proteins with a toxin, imageable
 CC compound or radionuclide. RetL1, optionally when expressed from
 CC vectors in vivo, is used to promote growth of new tissue and
 CC survival of damaged tissue, particularly kidney or neural tissue.
 CC Typical applications are in renal failure, nephritis, kidney
 CC transplants, toxic or hypoxic injury, neurodegeneration, motor
 CC neurone disease, multiple sclerosis, bacterial, viral or prion
 CC infections (e.g. meningitis, myelopathy associated with HIV or
 CC Creutzfeldt-Jakob disease), cranial nerve or spinal cord injury,
 CC developmental disorders such as Down's syndrome and cerebral palsy,
 CC or conditions involving the peripheral nervous system (Lyme
 CC disease, muscular dystrophy and myasthenia gravis). Fusion
 CC proteins are used to deliver toxins etc. to Ret-expressing cells,
 CC especially tumours.
 SO Sequence 3616 BP; 876 A; 955 C; 921 G; 864 T;
 Query Match 5.3%; Score 223; DB 39; Length 3616;
 Best Local Similarity 65.7%; Pred. No. 7.51e-126;
 Matches 592; Conservative 0; Mismatches 297; Indels 12; Gaps 8;

DB 694 acacattccaaaggaaacactgctgtgagcgaagcctgcaacctga...
 QY 2045 GGTACGCGGCAAGACACACATTTGCTGTGATGCTTCAAGGCTTCAACCTGATATCA...
 DB 754 ctgtaaagaagtaacaggtcgcgtatcacacccccctgca-ccaccagca-t-gtccaaaga
 QY 2105 CTGCAAGAAGCTGCGCTCCTCCTACATCTCATCTGCAACCGCGATCTGCCACCGA
 DB 811 ggtctgcaacccgccttaagtgcacaaagccctcagcagttcttcgacaaggttcgcg
 QY 2165 GCGCTGCAACCGCCGCAAGTGGCACAAAGGCCCTGGCGCATCTTCTGACCGGTCCAG
 DB 871 caagcagcgtacgggatgctcttctgctcctcgcggagacatgcctcaccagcgcg
 QY 2225 CGAGTACACCTTACCGCATGCTTTTGTCTCTCTCCCAAGNCCAGGCGTGGCTGACGCGC
 DB 931 gcgaagacatcgtcccggtgtgtctctatgaagaacgaagagagcgaactgctgag
 QY 2285 CCGCAACACATCTGCGCCAGCTGCTCTATGAGGACAAAGAGAACCCCACTGCTGGA
 DB 991 tctgcaagctcctcgaagaccatatacatctgcagatcctgcctcgaatttttctac
 QY 2345 CCGTGGTGGCGTGTCCGCACTGACACCTGTGTGGTCCCGCTGGCGGATTCATGC
 DB 1051 caactgcagcagagtcgaagttctgtgcacacactgtcttaagagaactacgacgactg
 QY 2405 CATTTGTGACGCTCTCTACACAGCGTCAACGCTGCTCGGCAATTCACAGCGTG
 DB 1111 cctctggtactcctgggagatgtatgacacagcagcagcctcacaactcgtatgactcag
 QY 2465 TGTGGGCTTTATGTGCTGGCATGATGGGTTTACATGACACTACTATGTGACTCCAG
 DB 1171 cagc-ct--cagcgtg---caacatgtgtatctgcagcagcagcgcgaatgactgga
 QY 2525 CCCCACTGGCATCTGGGTGTCCCTGTGTGACGTGTGTGACCGGCAACATGAGGA
 DB 1225 agactgctgaattcttgaattctttaaagacaactactgtctcaaaatgacaatga
 QY 2585 GAGGTGTGAGAGTCTCTACAGGACTTCAACGAGAACCATCTCTCCGAGCGCATCA
 DB 1285 agccttggcaatgtcctcagatgtacatgtgacgacgacccctcagtcacacacac
 QY 2645 GCGCTTGGCAACGGGACCAAGTGAAGTGTCCCAAAAGGCCCTGTTCCAGGCCAG
 DB 1345 c 1345
 QY 2705 C 2705

RESULT 6
 ID T84975 standard; cDNA: 2378 BP.
 AC T84975:
 DE 27-APR-1998 (first entry)
 DT Rat glial cell derived neurotrophic factor receptor alpha cDNA.
 KW Glial cell derived neurotrophic factor receptor alpha: GDNFR ;
 KW GDNF; rat; kidney disease; glomerulonephritis; therapy; ds.
 OS Rattus sp.
 FH key Location/Qualifiers
 FT CDS 117..1523
 FT sig_peptide 117..188
 FT mat_peptide 189..1520
 FT /tag= b
 FT /tag= c
 PD WO9733912-A2.
 PD 18-SEP-1997.
 PF 13-MAR-1997: U04363.
 PR 14-MAR-1996: US-618236.
 PR 14-MAR-1996: US-615902.
 PA (GENTECH) GENENTECH INC.
 PI Klein RD, Moore MM, Rosenthal A, Ryan AM;
 DR WPI: 97-470819/43.

1 P-PSDB:W27327.
 2 Isolated glial cell derived neurotrophic factor receptor alpha -
 3 useful to develop products to diagnose and treat associated
 4 disorders, particularly enteric nervous system or kidney disorders
 5 Claim 23: Page 74-77: 10pp: English.
 6 CC This cDNA codes for full-length rat glial cell derived neurotrophic
 7 factor receptor alpha (GDNFR alpha) (see W27327), a novel
 8 GPR-linked protein that is a ligand-binding component of the
 9 receptor system for GDNF. It was isolated by expression cloning.
 10 A cDNA library obtained from ventral midbrain tissue of E14 rat
 11 embryos was generated in a cytomegalavirus-based vector. cDNA
 12 clones were transfected into COS 7 cells and expression of
 13 putative GDNF receptors was detected by binding of iodinated GDNF.
 14 A single positive pool was obtained, from which the cDNA clone was
 15 isolated. An expression vector containing the cDNA can be used to
 16 produce GDNFR alpha in transformed host cells.
 17 relates to novel uses of GDNF and its receptor. The invention
 18 relates to novel uses of GDNF and its receptor. In particular, it
 19 relates to native rat GDNFR alpha (see W27327), its variants and
 20 soluble derivatives (extracellular domain), chimeric GDNFR alpha
 21 and antibodies which bind to the GDNFR alpha, including agonist
 22 and neutralising antibodies, as well as various uses for these
 23 molecules. It also relates to assay systems for detecting ligands
 24 CC to GDNFR alpha, systems for studying the physiological role of
 25 GDNF, diagnostic techniques for identifying GDNF-related conditions,
 26 methods for identifying molecules homologous to GDNFR alpha, and
 27 therapeutic techniques (claimed) for the treatment of GDNF-related
 28 CC and GDNFR alpha-related conditions, particularly kidney disease
 29 associated with glomerulonephritis and enteric nervous system
 30 related disorders. Transgenic and knockout animals are also
 31 claimed.
 32 Sequence. 2378 BP; 617 A.; 624 C; 598 G; 539 T;

Query Match	5.2%	Score 221	DB 37	Length 2378
Best Local Similarity	65.6%	Pred. 1,776-124		
Matches	591	Conservative	0	Mismatches 298; Indels 12; Gaps 8
Db	317	gcccagaagatagtcgcttaagcccatgtgaagcccttgaagaagaaagctctctgaactg	376	
Oy	1805	gcccacaaagagtggtccaggccgcttgtaggtgttcgagagagaccgctgtacgactg	1864	
Db	377	ccgctgcgaagcggggcatgaagaagaagaattgtctgcgtatctactctgagcatgta	436	
Oy	1865	ccgcgcgaagcgggggcgaagaagagactctcagctgttcgagatctactctgagacatcca	1924	
Db	437	ccagagcctt--c-aggaaatgacctctctgaaagattcccgtatgtgcggtctaaag	493	
Oy	1925	cctggcgctgacccaagsgtgaagactttacgaagaccctcccctatgacggcggtacttc	1964	
Db	494	caggttgcagatataattccggtgcagctccgtlcaatacagaatgtttccacaagtga	553	
Oy	1985	ccgcctctcggacatcttctcagggctgttccttcaatcttccagagagagggcgagaccggt	2044	
Db	554	acacattccaaagaaacaactgccttgaagcagcccaagccctgcgaacctgagcagac	613	
Oy	2045	ggtcagccccaagacaacacattgccttgatgctcccaagaccctgcacaacctgaatgacaa	2104	
Db	614	ctgtaaagaatgacagtgctgcgtacatcacaccctctga--ccaccaga--t-gtccaa	670	
Oy	2105	ctgcagaagagctggcgctctccttcatattccatctgcacaacggcagatctggccaccga	2164	
Db	671	ggtctgcacaccgctgaagtgcacaaagccctcaaggcagttcttcgaacaagtccgac	730	
Oy	2165	gcgcgtcgaacccggcgaagtgctccacaaagccctgcgcagattcttcgacccgggtccag	2224	
Db	731	caagagacagctaaaggaatgctctctctgtctctctgcggaatactgccttcacacggg	790	
Oy	2225	cgagtagacacccaacgcacatgctcttctgctctctgcacaaacacagccgtgcgtgacgcgcg	2284	
Db	791	gcgaagagctatgctccctcgctgctctctctgaagaacagagagggcccaactctgag	850	
Oy	2285	ccggcaaacatctctgcccactgctctctatgagagacaaagaaagcccaactctgctgga	2344	
Db	851	tctgcagaagctctctgcgaagacaaattatatactgcagaatctgcgcttgagaatttttac	910	

Oy	2345	CTGCGGTGCGCTGTGCGCGGACTGATGCCACTGTGTCTGCTGCCGCTCCGCGACTTCATTC	
Db	911	caactgccaagccagagatcaagatgctgtcagcaaatgctcttaagaagaactcaagcaatc	970
Oy	2405	CAATTGTGAGACCTTCATACCAAGAGGTCACACACTGCGCTCGGGACATTAACAAATCT	
Db	971	ctctcctgactactcctgagactgattggcaacagtcatgaatcccaactcaactcaactca	
Oy	2465	TCTGGGCTCTTATGCTGTGCATGATGTGGGTTGTGACATGACACCTTAATATGTGGT	
Db	1031	cagc-ct--cagcgtgg---cacacatggttgactcagcaaaagcagcgaatgcaatg	
Oy	2535	CCCACCTGGCATCTGTGTGTCTCCCTGTGTGTCACCTGTCTGTGGCAGCGGGAACATG	
Db	1085	agactgcttgaataattctgaattttttaaagaacaatactgtctcaaaaatgcaatlca	
Oy	2585	GGAGTGTGAGAAAGTTCTCTCAAGGGAGCTTCACCGAAGAACCATGCTTCGGGAAGCATCA	257
Db	1145	agccttggcaaatgagctcagaatgtgacacatgtgagccagccctcagatccagaagc	1200
Oy	2645	GCGCTTTGGCGAACGCGCACGAAACGTGATCCCAAAAGGCCCTCTCTTCAGGCGCAC	2700
Db	1205	c 1205	
Oy	2705	c 2705	
RESULT	7		
ID	T88419	standard: cDNA: 2568 BP.	
AC	T88419		
DT	01-MAY-1998	(first entry)	
DE	Human glial cell line-derived neurotrophic factor receptor cDNA.		
KW	Human; glial cell line-derived neurotrophic factor; GDNF; receptor;		
KW	treatment; dopaminergic nerve cell disorder; Parkinson's disease;		
KW	Alzheimer's disease; amyotrophic lateral sclerosis; diabetes;		
KW	Huntington's disease; glaucoma; retinal degeneration; hearing loss;		
KW	gene therapy; ss.		
OS	Homo sapiens.		
FT	Key	Location/Qualifiers	
FT	CDS	540..1937	
FT		/tag= a	
FT		/product= GDNF_receptor	
PN	W09740152-A1.		
PD	30-OCT-1997.		
PF	15-APR-1997.	U06281.	
PR	14-APR-1997.	US-837199.	
PR	22-APR-1996.	US-015907.	
PR	09-MAY-1996.	US-017221.	
PA	(AMGE-) AMGEN INC.		
PI	Fox GM, Jing S, Men D.		
DR	WPI: 97-535836/49.		
DR	P-PSDB: W35333.		
PT	glial cell line derived neurotrophic factor receptor - useful to		
PT	glial cell line derived neurotrophic factor receptor - useful to		
PT	Alzheimer's disease		
PS	Claim 17: Pages 91-93, 196pp: English.		
CC	The present sequence encodes the human glial cell line-derived		
CC	neurotrophic factor (GDNF) receptor, which can be used to treat		
CC	dopaminergic nerve cell disorders, e.g. Parkinson's and Alzheimer's		
CC	disease or amyotrophic lateral sclerosis, complications of diabetic		
CC	and Huntington's disease and (optionally in combination with GDNF)		
CC	glaucoma, retinal degeneration and hearing loss caused by injury to		
CC	inner ear sensory neurons. The receptor can also be used to block		
CC	unwanted GDNF activity, analyse GDNF related molecules and		
CC	stabilise GDNF in pharmaceutical formulations. Receptor expression		
CC	cells, preferably transfected ex vivo, can be used similarly to		
CC	implantation, and the use of the receptor cDNA in gene therapy		
CC	also contemplated. Probes based on the cDNA can be used to identify		
CC	GDNF responsive cells and tissues, e.g. to identify patients who		
CC	would benefit from GDNF therapy, and abnormalities in receptor		
CC	expression, and to isolate molecules that form a complex with the		
CC	cDNA or are homologous/cross-reactive with the cDNA. Anti-sense		
CC	cDNA or are homologous/cross-reactive with the cDNA. Anti-sense		

KW GDNF: human; kidney disease; glomerulonephritis; therapy; EST;
KM expressed sequence tag; ss.
OS Homo sapiens.
PN M09733912-A2.
PD 18-SEP-1997.
PR 13-MAR-1997; U04363.
PR 14-MAR-1996; US-618236.
PR 14-MAR-1996; US-615902.
PA (GENE) GENENTECH INC.
PI Klein RD, Moore MW, Rosenthal A, Ryan AM;
DR WPI: 97-470819/43.
PT Isolated glial cell derived neurotrophic factor receptor alpha -
PT useful to develop products to diagnose and treat associated
PT disorders, particularly enteric nervous system or kidney disorders
PS Example 1: Page 61; 100pp; English.
CC This DNA sequence comprises a fragment of a human EST-derived
CC sequence designated Y170a10.r1 (see T84979). It can be used as
CC a probe to identify glial cell derived neurotrophic factor receptor
CC (GDNFR) sequences, including human variants. The invention relates
CC to novel uses of GDNF and its receptor. In particular, it relates
CC to rat GDNFR alpha (see W27327), its variants and soluble derivatives
CC (extracellular domain), chimeric GDNFR alpha and antibodies which
CC bind to the GDNFR alpha, including agonist and neutralising
CC antibodies, as well as various uses for these molecules. It also
CC relates to assay systems for detecting ligands to GDNFR alpha,
CC systems for studying the physiological role of GDNF, diagnostic
CC techniques for identifying GDNF-related conditions, methods for
CC identifying molecules homologous to GDNFR alpha, and claimed
CC methods for the treatment of GDNF-related and GDNFR alpha-related
CC conditions, particularly kidney disease associated with
CC glomerulonephritis and enteric nervous system related disorders.
CC Transgenic and knockout animals are also claimed.
SQ Sequence 201 BP; 41 A; 78 C; 46 G; 36 T;

Query Match 4.7%; Score 201; DB 37; Length 201;
Best Local Similarity 100.0%; Pred. No. 6.05e-111;
Matches 201; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 gcaacattgctgtagtctgcaagagctgcaactgaaatgacactgcaagaagctgc 60
|||
Oy 2059 GCAACATTGCTGATGCTGCAAGGCTGCACTGAAATGACAAAGCAAGAGCTGC 2118
|||
Db 61 gctctctacatctccatctgcaacgcgagatctgcccacgcgagctgcaacgccc 120
|||
Oy 2119 GCTCTCTACATCTCCATCTGCAACCGCGAATCTGCCCCACCGAGGCTGCCAACCCGCC 2178
|||
Db 121 gcaagtcgcaagaagccctgcgcagcttcttcgacgcggtgcccagcgaagtaacctacc 180
|||
Oy 2179 GCAATGCGCACAGGCGCTGCGCCAGTTCTTGACGGGTGCCGACGAGTACACTAC 2238
|||
Db 181 gcatgctcttctgctcctgccc 201
|||
Oy 2239 GCATGCTCTCTGCTGCTGCTGCC 2259

RESULT 10
ID V00246 standard; cDNA; 1223 BP.
AC V00246;
DT 21-MAY-1998 (first entry)
DE Human Ret ligand retl1 partial cDNA.
KW Ret ligand; RetL; receptor; signal transduction; human;
KW cell growth; renal cell; nerve cell; renal failure; nephritis;
KW kidney transplant; toxic injury; hypoxic injury;
KW neurodegeneration; motor neurone disease; multiple sclerosis;
KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
KW cranial nerve injury; spinal cord injury; Down's syndrome;
KW cerebellar palsy; Lyme disease; muscular dystrophy;
KW myasthenia gravis; tumour; therapy; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..1041
FT CDS /*tag= a
PN M09744356-A2.

PD 27-NOV-1997.
PF 07-MAY-1997; U07726.
PR 10-APR-1997; US-017427.
PR 08-MAY-1996; US-017427.
PR 07-JUN-1996; US-019300.
PR 16-JUL-1996; US-021859.
PA (BIO) BIOGEN INC.
PI Cate RL, Heslop C, Santicola-Nadel M;
DR WPI: 98-018431/02.
DR P-PSDB: M37458.
PT New nucleic acid encoding ret receptor ligands and related proteins
PT - vectors, transformed cells and antibodies, used for promoting cell
PT growth and improving survival of injured cells, especially renal or
PT nerve cells
PS Claim 1: Page 58-60; 113pp; English.
CC This sequence comprises a partial cDNA for human Ret ligand (RetL)
CC RetL (see M37458), a key component of the Ret signalling pathway.
CC It was isolated from a human embryonic kidney cDNA library using
CC rat RetL cDNA (see V00245) as probe. A full-length sequence (see
CC V00247) for human RetL cDNA has also been obtained, as well as
CC mouse and human RetL2 and RetL3 sequences (see V00248-51). Vectors
CC containing RetL DNA and prokaryotic or eukaryotic host cells
CC transformed or transfected with these vectors are claimed, as well
CC as a method for production of RetL. Its soluble variants and
CC fusion proteins with a toxin, imageable compound or radionuclide,
CC RetL, optionally when expressed from vectors in vivo, is used to
CC promote growth of new tissue and survival of damaged tissue,
CC particularly kidney or neural tissue. Typical applications are in
CC renal failure, nephritis, kidney transplants, toxic or hypoxic
CC injury, neurodegeneration, motor neurone disease, multiple
CC sclerosis, bacterial, viral or prion infections (e.g. meningitis,
CC myelopathy associated with HIV or Creutzfeldt-Jakob disease),
CC cranial nerve or spinal cord injury, developmental disorders such
CC as Down's syndrome and cerebral palsy, or conditions involving
CC peripheral nervous system (Lyme disease, muscular dystrophy, etc.
CC myasthenia gravis). Fusion proteins are used to deliver
CC etc. to Ret-expressing cells, especially tumours.
SQ Sequence 1223 BP; 323 A; 329 C; 274 G; 297 T;

Query Match 3.8%; Score 161; DB 39; Length 1223;
Best Local Similarity 65.6%; Pred. No. 4.53e-84;
Matches 434; Conservative 0; Mismatches 219; Indels 5;

Db 89 ccaaaaggaaacactgctgtagtgcaggaagagctgcaactgcagacattgcaaa 120
|||
Oy 2053 CCAAGACCAACATTGCTGCTGATGCTGCCAAGGCTGCACTGAAATGACAACTGCAAGA 2118
|||
Db 149 agtcagtgctgggtatatacaaccgcgtgca-ccacagcg-t-gtccaaagatgctcgtg 200
|||
Oy 2113 AGTGGCTCTCTCTACATCTCCATCTGCAACCGCGAATCTGCCCCACCGAGCTGCTGA 2178
|||
Db 206 accgcgcgaagtcgcaagaagccctgcgcagcttcttcgcaagagctccgcgaag 2118
|||
Oy 2173 ACCGCCGCAAGTGCACAAAGGCGCTGCGCCAGTTCTTGACACGGGTGCCACAGTCA 2238
|||
Db 266 gctacggaatgctcttctgctcctgcgcgagacatgcctgcgacagcgagagcga 2718
|||
Oy 2233 CCAACCGCAAGTGCCTTCTGCTGCTGCGCCAAAGACAGGCGTGGTACGCGCGCGCAAA 2293
|||
Db 326 ccaatcgagctgtgtgctctctatgaagaagggagagcccaactgttttaattgca 2303
|||
Oy 2293 CCATCCGCGCCCAAGTGTCTCTATGAGACCAAGGAGGAGCCCACTGCTGAGCTGCTG 2353
|||
Db 386 actcctgcaagaagcaatatacatctgcagatctgcgccttgagatttttaccacacg 2412
|||
Oy 2353 GCGTGTGCGGAGCTGACACACTGTGTGCTGCGGCTGCGGCTGCTGCAATTCATGCA 2472
|||
Db 446 agcagaagtaaggtctgtcagcagcgtgtctaaaggaanaactacgtctgactcct 505
|||
Oy 2413 GAGCGCTCTACACAGAGGTGACACAGCTGCGCTGGGAGCAATTACAGGCTGTCTGGCG 563
|||
Db 506 cctactcgaggctattatggcagcagtcatacccccacacatagactcagtagc-ct- 563
|||

QY 2473 CTTATCTGCGATGATTGGTTGACATGACACCTACTATGTGACTCCAGCCACATG 2532
 Db 564 -ca--gtg--tggcccatggtgactgacgacacagtgagaaagcctagaagatgct 619
 QY 2533 GCATCTGTGGTCCCTCCCTGTGTCAGTGTCTGTCAGCGGAAACATGAGAGATGTG 2592
 Db 620 tgaatttttgaattcttcctcaagacaatacatatgcttaaaatgcaatccaagcttg 679
 QY 2593 AGAAGTTCCTCAGGACTTCACGAGAACCCATGCTCCGGAAAGCGCATCCAGGCTTTG 2652
 Db 680 gcaatgctccgactgacgctgtgacgacacccctcccaagacagaccacacacgca 739
 QY 2653 GCACACGCGACGACGATGTAACGTGTCCCAAAAGGCCCTCTTCCAGCGCACCCAGGCC 2712
 Db 740 ct 741
 QY 2713 CT 2714

RESULT 11
 ID V00247 standard; cDNA: 1682 BP.
 AC V00247:
 DT 21-MAY-1998 (first entry)
 DE Human Ret ligand retL cDNA.
 KW Ret ligand; RetL; receptor; signal transduction; human;
 KW cell growth; renal cell; nerve cell; nerve failure; nephritis;
 KW kidney transplants; toxic injury; hypoxic injury;
 KW neurodegeneration; motor neurone disease; multiple sclerosis;
 KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
 KW cranial nerve injury; spinal cord injury; Down's syndrome;
 KW cerebellar palsy; Lyme disease; muscular dystrophy;
 KW myasthenia gravis; tumour; therapy; ss.
 OS Homo sapiens.
 FH Key
 FT CDS location/Qualifiers
 FT 118..1500
 FT /tag= a
 PN W09744356-A2.
 PD 27-NOV-1997.
 PE 07-MAY-1997: U07726.
 PR 10-APR-1997: US-017427.
 PR 08-MAY-1996: US-017427.
 PR 07-JUN-1996: US-019300.
 PR 16-JUL-1996: US-021859.
 PA (BioJ) BIOGEN INC.
 PI Cate RL, Hession C, Sanicola-Nedel M:
 DR MPI: 98-018431/02.
 P-PSDB: W37459.
 PT New nucleic acid encoding ret receptor ligands and related proteins.
 PT - vectors, transformed cells and antibodies, used for promoting cell
 PT growth and improving survival of injured cells, especially renal or
 PT nerve cells
 PS Claim 1: Page 62-64: 113pp: English.
 CC This sequence comprises cDNA coding for human Ret ligand (RetL)
 CC RetL (see W37459), a key component of the Ret signalling pathway.
 CC It was deduced from 2 clones isolated from human foetal kidney
 CC cDNA using primers based on a partial human retL cDNA (see
 CC V00246). Rat retL and mouse and human retL2 and retL3 sequences
 CC have also been identified (see V00245 and V00248-51). The human
 CC retL cDNA is 88.2% identical to rat retL cDNA. Vectors
 CC containing retL DNA and prokaryotic or eukaryotic host cells
 CC transformed or transfected with these vectors are claimed, as well
 CC as a method for production of RetL, its soluble variants and
 CC fusion proteins with a toxin, imageable compound or radionuclide.
 CC RetL, optionally when expressed from vectors in vivo, is used to
 CC promote growth of new tissue and survival of damaged tissue,
 CC particularly kidney or neural tissue. Typical applications are in
 CC renal failure, nephritis, kidney transplants, toxic or hypoxic
 CC injury, neurodegeneration, motor neurone disease, multiple
 CC sclerosis, bacterial, viral or prion infections (e.g. meningitis,
 CC myelopathy associated with HIV or Creutzfeldt-Jakob disease),
 CC cranial nerve or spinal cord injury, developmental disorders such
 CC as Down's syndrome and cerebral palsy, or conditions involving the
 CC peripheral nervous system (Lyme disease, muscular dystrophy and

CC myasthenia gravis). Fusion proteins are used to deliver
 CC etc. to Ret-expressing cells, especially tumours.
 SQ Sequence 1682 BP; 417 A; 461 C; 433 G; 371 T;
 Query Match 3.8%; Score 161; DB 39; Length 1682;
 Best Local Similarity 65.6%; Pred. No. 4,536-84;
 Matches 434; Conservative 0; Mismatches 219; Indels 9; Gaps

Db 548 ccaaaagggaacacacgctgcatgaggaagagcctgtaaacctgacacattgcaaa 607
 QY 2053 CCAAGAGCAACCATTTGCTTGATGCTGCAAGGCTGCAACCTGATACACTGCACAGA 2112
 Db 608 agtaacagtcgacgacatcaaccccgatga--ccaacagc--t--gtccacagatgtcga 604
 QY 2113 AGCTGGCTCCCTCCATCATCTCATCTGCACACCGGAGATCTCGCCACCGAGCGTGA 2172
 Db 665 accgcgcgaagtgcacaaagccctcgagcttccttgacaagagtcgcgcgaagcaca 724
 QY 2173 ACCGCCGCAAGGCGCACAGGCCCTCGCCAGTTCTTGACCGGCTGCCAGCGAGTACA 2232
 Db 725 gctacgaatgctcttctgctcctgacgagacatgctgacagagcggagcgacaga 784
 QY 2233 CTTACCGCATGCTCTTGTGCTCTGCAAGACCAAGCGTGGCTGAGCGCGCGCAAA 2292
 Db 785 ccacgtgcctgtgtgctcctcaagaagaggaagaccccaactgtttgaattgcag 844
 QY 2293 CCATCTCCGCCAGCTGCTCTCATGAGACAGAGAACCCCACTGCTGACCTGCTG 2352
 Db 845 actcctgaagaagcaattacatctgcagatctgccttgcgattttttaccacactgc 904
 QY 2353 GCGTGTGCGGACTGACACCATCGTGTGCGGCTGCGGCTGCGGACTTCATCGCAATTGTC 2412
 Db 905 agccagagtcacagctctgtcagcagctgtcctaaagaaactacgctacgctccctcg 964
 QY 2413 GAGCTCTCACCAGACGGTCAACACAGCTCCCTGCGGCAATTAACAGCGCTGTGGCT 2472
 Db 965 cctactcggggtctatctgacacagtcacagccccaactacatagacacagtagc--ct- 1022
 QY 2473 CTTATGTCGGCATGATTTGGTTTGACATGACACCACTAATATGTGACTCCAGCCCATG 2532
 Db 1023 -ca--gtg--tggcccatggtgactgacgacacagtgagaaagcctagaagatgct 1078
 QY 2533 GCATGTGTGTGTCCTCCCTCGTGTGACGTCTGTGCGGACCGGACATGAGAGAGTGTG 2592
 Db 1079 tgaatttttgaattcttcctcaagacaatacatatgcttaaaatgcaatccaagcttg 1148
 QY 2593 AGAAGTTCCTCAGGACTTCACCGAGAACCCATGCTCCGGAACGCCATCCAGCGCTTTG 2652
 Db 1139 gcaatgctccgactgacgctgtgacgacacccctcccaagtaacagaccacactgcga 1198
 QY 2653 GCACGCGCACGACGTGAAGTGTCTCCCAAAAGGCCCTCTTCCAGGCGCACCGAGCTC 1258
 Db 1199 ct 1200
 QY 2713 CT 2714

RESULT 12
 ID T84977 standard; cDNA: 840 BP.
 AC T84977:
 DT 27-APR-1998 (first entry)
 DE Mouse GDNF alpha clone 26.3' end.
 KW GDNF; mouse; kidney disease; glomerulonephritis; therapy; ss.
 OS Mus musculus.
 PN W09733912-A2.
 PD 18-SEP-1997.
 PE 13-MAR-1997: U04363.
 PR 14-MAR-1996: US-618936.
 PR 14-MAR-1996: US-618936.
 PA (GERT) GENENTECH INC.
 PI Klein RD, Moore MM, Rosenthal A, Ryan AM:
 DR MPI: 97-470819/43.

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 W37460 (TM)

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Search - protein database search, using Smith-Waterman algorithm

Run on: Mon Mar 8 14:01:32 1999; Maspar time 16.46 Seconds

Tabular output not generated. 455.994 Million cell updates/sec

Title: >US-08-866-354-36
 Description: (1-464) from US08866354.pep
 Perfect Score: 3386
 Sequence: 1 MILANVFCLFFLDLTLRL.....RAPSALTVLSVLMKRL 464

Scoring table:
 PAM 150
 Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database:

a-geneseq32
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19 20:part20 21:part21 22:part22 23:part23
 24:part24 25:part25 26:part26 27:part27 28:part28
 29:part29

Statistics: Mean 34.889; Variance 136.192; scale 0.256

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	3383	99.9	464	W37460	Human Ret ligand RetL	0.00e+00
2	1554	45.9	466	W35334	Rat glial cell line-d	2.14e-152
3	1554	45.9	466	W37457	Rat Ret ligand RetL	2.14e-152
4	1554	45.9	466	W27327	Rat glial cell line	2.14e-152
5	1520	44.9	465	W35333	Human glial cell line	1.09e-148
6	1499	44.3	460	W37459	Human Ret ligand RetL	2.11e-146
7	1142	33.7	346	W37458	Human Ret ligand RetL	1.28e-107
8	782	23.1	397	W37461	Mouse Ret ligand RetL	7.23e-69
9	755	22.3	346	W37455	Mouse Ret ligand RetL	5.53e-66
10	708	20.9	400	W37463	Human Ret ligand RetL	5.64e-61
11	676	20.0	315	W37462	Human Ret ligand RetL	3.42e-57
12	103	3.0	1712	W22461	Masking protein high	8.62e-00
13	98	2.9	179	W21646	Gravidine leucidin v1	7.20e+00
14	99	2.9	483	R15509	Tomato ACC synthase	7.20e+00
15	99	2.9	4472	W22601	Tyrosine synthase OR	7.20e+00
16	95	2.8	402	R06485	Beta 3 adrenergic rec	1.47e+01
17	95	2.8	408	R54991	Human beta-3 adrenergic	1.47e+01
18	91	2.7	342	R12089	Antigenic cysteine pro	2.97e+01

19	91	2.7	342	R12090	Antigenic cysteine pro	2.97e+01
20	93	2.7	485	R15508	Tomato ACC synthase e	2.09e+01
21	88	2.6	227	R04497	HIV fusion protein PB	4.98e+01
22	88	2.6	227	P94807	Pblm12 HIV fusion pr	4.19e+01
23	89	2.6	325	R91347	Murine PLAP, for redu	4.19e+01
24	89	2.6	325	R85872	MD-40 domain-contg. P	4.19e+01
25	89	2.6	325	R25074	PLAP	4.19e+01
26	89	2.6	362	R48695	G-protein coupled hum	4.19e+01
27	89	2.6	362	W02667	G-protein coupled hum	4.19e+01
28	88	2.6	520	R52831	Sequence of human alp	4.19e+01
29	87	2.6	520	R53072	Alpha 1b adrenergic r	4.19e+01
30	87	2.6	520	R85943	Alpha 1b adrenergic r	4.19e+01
31	89	2.6	814	W11940	gd.trkA fusion us	4.19e+01
32	88	2.6	925	R79148	Human insulin recepto	4.19e+01
33	89	2.6	1404	R38304	Sequence of a serin	4.19e+01
34	86	2.5	226	R13757	Prolectin	4.19e+01
35	84	2.5	240	W23954	Chimeric humanised m	4.19e+01
36	85	2.5	650	P81137	Human protein S	4.19e+01
37	84	2.5	751	R53088	Human masking protein	4.19e+01
38	84	2.5	752	R53087	Human masking protein	4.19e+01
39	84	2.5	756	R53086	Human masking protein	4.19e+01
40	85	2.5	843	R27744	Extracellular protein	4.19e+01
41	84	2.5	845	R53089	Human masking protein	4.19e+01
42	84	2.5	1355	R14584	TGF beta 1 binding pr	4.19e+01
43	84	2.5	1830	R44504	Urea amide lyase.	4.19e+01
44	85	2.5	4544	R60517	Human alpha-2-MR.	4.19e+01
45	85	2.5	4544	R47861	Alpha 2-Macroglobulin	4.19e+01

ALIGNMENTS

RESULT 1
 ID W37460 standard; Protein: 464 AA.

AC W37460; (first entry)

DE 21-MAY-1998

DI Human Ret ligand RetL2.

KW Ret ligand; RetL; RetL2; receptor; signal transduction; human;

KW cell growth; renal cell; nerve cell; renal failure; nephritis;

KW kidney transplants; toxic injury; hypoxic injury;

KW neurodegeneration; motor neurone disease; multiple sclerosis;

KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;

KW cranial nerve injury; spinal cord injury; Down's syndrome;

KW cerebral palsy; Lyme disease; muscular dystrophy;

KW myasthenia gravis; tumour; therapy.

OS Homo sapiens.

PN W09744356-A2.

PD 27-NOV-1997

PE 07-MAY-1997; U07726.

PR 10-APR-1997; US-017427.

PR 08-MAY-1996; US-017427.

PR 07-JUN-1996; US-019300.

PR 16-JUL-1996; US-021859.

PA (Bio) BIOGEN INC.

PI Cate RL, Hesslon C, Santicola-Nadel M;

DR N-PSDB: W00248.

DR N-PSDB: W00248.
 New nucleic acid encoding ret receptor ligands and related proteins
 - vectors, transformed cells and antibodies, used for promoting cell
 growth and improving survival of injured cells, especially renal or
 nerve cells
 PS Claim 2: Page 69-70; 113pp: English.
 CC This amino acid sequence comprises human Ret ligand (RetL) RetL2.
 CC deduced from a cDNA clone (see W00248) isolated from a human foetal
 CC liver library. Ret and human RetL1, and human and mouse RetL
 CC sequences (see W37457-59 and W37461-63) are also claimed. Human
 CC RetL2 is 49.1% identical to human RetL protein. RetL is a
 CC key component of the Ret signalling pathway that specifically
 CC interacts with Ret receptor protein, triggering Ret dimerisation
 CC and/or autophosphorylation of the Ret tyrosine kinase domain.
 CC Vectors containing RetL2 DNA and prokaryotic or eukaryotic host
 CC cells transformed or transfected with these vectors are claimed, as
 CC well as a method for production of RetL2, its soluble variants and
 CC fusion proteins with a toxin, imageable compound or radionuclide.

CC Reti2, optionally when expressed from vectors in vivo, is used to
 CC promote growth of new tissue and survival of damaged tissue,
 CC particularly kidney or neural tissue. Typical applications are in
 CC renal failure, nephritis, kidney transplants, toxic or hypoxic
 CC injury, neurodegeneration, motor neurone disease, multiple sclerosis,
 CC bacterial, viral or prion infections (e.g. meningitis, myelopathy
 CC associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
 CC spinal cord injury, developmental disorders such as Down's syndrome
 CC and cerebral palsy, or conditions involving the peripheral nervous
 CC system (Lyme disease, muscular dystrophy and myasthenia gravis).
 CC Fusion proteins are used to deliver toxins etc. to Ret-expressing
 CC cells, especially tumours.
 CC Sequence 464 AA:

Query Match 99.9%; Score 3383; DB 28; Length 464;
 Best Local Similarity 99.6%; Pred. No. 0.00e+00;
 Matches 462; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 1 mlanafeclffideltislaaspslqgpehlywvrvpvcvranelcaaeenccsarytl 60
 Qy 1 mlanafeclffideltislaaspslqgpehlywvrvpvcvranelcaaeenccsarytl 60
 Db 61 rclclgrdntmlankekcaalevlyqesplydcrcrkqmkkelqclqylwshlqtege 120
 Qy 61 rclclgrdntmlankekcaalevlyqesplydcrcrkqmkkelqclqylwshlqtege 120
 Db 121 efyeaspyevvrsrlsdifrlasifsgtadpvyasakshncidaekacnlndncklirs 180
 Qy 121 efyeaspyevvrsrlsdifrlasifsgtadpvyasakshncidaekacnlndncklirs 180
 Db 181 ylsicnreislptercnrrckhkalrqqfdvpselyrmlfscqdgacaeerrigtlips 240
 Qy 181 ylsicnreislptercnrrckhkalrqqfdvpselyrmlfscqdgacaeerrigtlips 240
 Db 241 cseyekexpncldlrgvctdhlcrsladfnancrasqvtscpadnygcslsygm 300
 Qy 241 cseyekexpncldlrgvctdhlcrsladfnancrasqvtscpadnygcslsygm 300
 Db 301 lqfdmtpyvdspglvsvpcscrgsqmneecckflrfttencprlnaiafgnqtd 360
 Qy 301 lqfdmtpyvdspglvsvpcscrgsqmneecckflrfttencprlnaiafgnqtd 360
 Db 361 vnvspkgsfqtqgprvexkpslpddlsdstslgsvlctctavqegglkannskelam 420
 Qy 361 vnvspkgsfqtqgprvexkpslpddlsdstslgsvlctctavqegglkannskelam 420
 Db 421 cfteltlnlpgsnkvikpnsgrsraipsaalvtlsvlmklal 464
 Qy 421 cfteltlnlpgsnkvikpnsgrsraipsaalvtlsvlmklal 464

RESULT 2
 ID W35334 standard; Protein: 468 AA.
 AC W35334.
 DT 01-MAY-1998 (first entry)
 DE Rat glial cell line-derived neurotrophic factor receptor.
 KW Rat; glial cell line-derived neurotrophic factor; GDNF; receptor;
 KW treatment; dopaminergic nerve cell disorder; Parkinson's disease;
 KW Alzheimer's disease; amyotrophic lateral sclerosis; diabetes;
 KW Huntington's disease; glaucoma; retinal degeneration; hearing loss;
 KW gene therapy.
 OS Rattus sp.
 PN M09740152-A1.
 PD 30-OCT-1997.
 PE 15-APR-1997; U06281.
 PR 14-APR-1997; U06281.
 PR 22-APR-1996; U06281.
 PR 09-MAY-1996; U06281.
 PA (AMGE-) AMGEN INC.
 PI Fox GM, Jang S, Men D;
 DR WPI: 97-535836/49.
 DR N-PSDB: T95297.
 PT Glial cell line derived neurotrophic factor receptor - useful to

PT treat dopaminergic nerve cell disorders, e.g. Parkinson's and
 PT Alzheimer's disease.
 PS Claim 1: Pages 96-98: 196pp: English.
 CC The present sequence is the rat glial cell line-derived
 CC neurotrophic factor (GDNF) receptor, which can be used to treat
 CC dopaminergic nerve cell disorders, e.g. Parkinson's and Alzheimer's
 CC disease or amyotrophic lateral sclerosis, complications of diabetes
 CC and Huntington's disease and (optionally in combination with GDNF)
 CC glaucoma, retinal degeneration and hearing loss caused by injury to
 CC inner ear sensory neurons. The receptor can also be used to block
 CC unwanted GDNF activity, analyse GDNF related molecules and
 CC stabilise GDNF in pharmaceutical formulations. Receptor expressing
 CC cells, preferably transfected ex vivo, can be used similarly by
 CC implantation, and the use of the receptor cDNA in gene therapy is
 CC also contemplated. Probes based on the cDNA can be used to identify
 CC GDNF responsive cells and tissues, e.g. to identify patients who
 CC would benefit from GDNF therapy, and abnormalities in receptor
 CC expression, and to isolate molecules that form a complex with the
 CC cDNA or are homologous/cross-reactive with the cDNA. Anti-receptor
 CC antibodies, oligonucleotides derived from the cDNA and animal
 CC models that overexpress the receptor can be used to study the
 CC biological function of GDNF, knockout transgenic animals can be
 CC used to detect GDNF dependent neurons or processes and the anti-
 CC can be used in immunoassays for the receptor. The receptor can be
 CC GDNF specifically and with high affinity, acting as part of a
 CC complex that mediates/enhances signal transduction by GDNF.
 CC Increasing dopamine uptake in dopaminergic cells.
 CC Sequence 468 AA:

Query Match 45.9%; Score 1554; DB 28; Length 468;
 Best Local Similarity 48.2%; Pred. No. 2.14e-152;
 Matches 223; Conservative 102; Mismatches 120; Indels 36;

Db 2 flatiyfalpldlimeevsg-gdrldcvvasdqclkegscstkytltrcvagkknv 4
 Qy 12 fludturlaspslqgclgwmrppvdcvranelcaaeenccsarytlrclclgrdnt 7
 Db 61 slsgleakdecrasamealxkgslyncrcrkqmkkelcnclrlymsygal-qgnldleds 119
 Qy 71 tm---lank-bcqaalevlyqesplydcrcrkqmkkelcldciywsihlqtegefevns 120
 Db 120 pyepvnsrlsdifrafvfscvqvehlsgknncldaekacnlndncklirsytlips 120
 Qy 127 pyepvnsrlsdifrafvfscvqvehlsgknncldaekacnlndncklirsytlips 120
 Db 180 tsmv-nevncrrckhkalrqqfdvpselyrmlfscqdgacaeerrigtlips 180
 Qy 187 reispkerckhkalrqqfdvpselyrmlfscqdgacaeerrigtlips 187
 Db 239 erpnclslqgackcnylcrsladffncqpsrsvancnklenyadcllaysgllqctvm 239
 Qy 247 EKPNCIDLRGVCRTDHLCRSLADFNANCRASYTIVSCPADNYGC SLGAGMIGDH 247
 Db 299 pnyvds-s-lsvapwcdcsngndledclflnfikntclxnaiafgnsdvcmwyp 356
 Qy 307 PNYVDSPTGLVSPMCSRGSGMNEECCKFLRFTTENCPRLNIAIAFGNGTWNVSPK 346
 Db 357 appqcttattatfrknkplgpageneplthlpncanlgqklkxvsgthclsls 416
 Qy 367 GPSFOATQAPRV-E-KTPSLDDLSSTS-IGSVITTCSTVOROGKANNKSKELSMCFT 423
 Db 417 dsdfgkdglagasehltks-ma-appscslslypmltala 457
 Qy 424 E-LTTNIIPOSNKVIRKPNSGPSRARPSAALTIVSLMLKLAL 463

RESULT 3
 ID W37457 standard; Protein: 468 AA.
 AC W37457.
 DT 21-MAY-1998 (first entry)
 DE Rat Ret ligand Reti1.
 KW Rat Ret ligand; Reti1; receptor; signal transduction; rat;
 KW cell growth; renal cell; nerve cell; renal failure; nephritis;

[illegible][illegible]

Query Match 1554; Score 1554; DB 27; Length 468;
Best Local Similarity 48.9%; Pred. No. 2,14e-152;
Matches 223; Conservative 102; Mismatches 120; Indels 18; Gaps 15

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Dd      2 flatlyfplpldlmsaevsq-gdrldcvksdqclkegscktyrltvgvagnefn 60  
       || :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
Oy     12 FLDDTLRLSLASPSSLOGGELHGMRPVDCVANELLCAENSCSSRYRLLRGCLAGDRN- 70  
       ::||::||::||::||::||::||::||::||::||::||::||::||::||::||  
Dd      61 slstgleakdecreamealxgkslyncrcrkgmkekncultllysmysgl-qgnadlleds 119  
       ::||::||::||::||::||::||::||::||::||::||::||::||::||::||  
Oy      71 TM--LARK-CCQAALLEVLAQESPLYDCCKSGMKRELOCLOIYWSIHGLGEGEFEYAS 126  
       ::||::||::||::||::||::||::||::||::||::||::||::||::||::||  
Dd     120 pypenrsldgfrravpfisdfvgvehlskqmcldaekacnldcttkyrasytpct 179  
       ||||| ||||| ||||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
Oy     127 PYEPVTSLSLSTIFRLASTFSFGTGADPVVASNSNHCDAARACNLNDNCKKLRSSYISCN 186  
       ||||| ||||| ||||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
Dd     180 tsm-s-necvnrcrkchkalrgfdfkvpahkysgmalfscgrdiacterrqtltvpcsyeeer 238  
       || :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
Oy     187 REISPTECNKRKKCKAKLRGFEDRPSPSYTRYRMFLFCSDODACAERRQTILLPSCSYEDK 246  
       ::||::||::||::||::||::||::||::||::||::||::||::||::||::||  
Dd     239 erpnclsldgcktnylsrsladflfncgpssrsvsnclkenyadcllaysgligtwtmt 298  
       ||:|||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
Oy     247 EKPNCILDRGVCRTHDLCSRSLADFHANCRASYOTVTWSCPADNYQACIGSAYAGICFDMT 306  
       ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Dd     229 pnydds-s-lsvpmwccnsngndledcflnfiffhdntlkhaifagfsavtmqp 356  
       ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Oy     307 PNYVDSSPTGTIVSPWCSRCGSNGMECEKFLEDFENPCPLRNAIOAFGGTVVANSPPK 366  
       ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Dd     357 appvqtattcttafrvxnkpdpagseneipthvlppcanldgaqklksnvsghclsls 416  
       ::||::||::||::||::||::||::||::||::||::||::||::||::||::||  
Oy     367 GPSQATQAPRV-E-KTPSLPDLDSDRS-LGTSVITTCSTVSQGOLKANNRKSLSCFT 423  
       ::||::||::||::||::||::||::||::||::||::||::||::||::||::||  
  
Db     417 dsdfgkdglagasshlctks-ma-appscsissjpvmltala 457  
       :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
Oy     424 E-LTTNIIPGSNMVKIKENSGPSRAPFAALTVLVIMLK-LA 463  
       :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
  
RESULT          5  
ID W35333 standard; Protein; 465 AA.  
AC W35333;  
DT 01-MAY-1998 (first entry)  
DE Human glial cell line-derived neurotrophic factor receptor.  
KW Human: glial cell line-derived neurotrophic factor; GDNF; receptor;  
   treatment; dopaminergic nerve cell disorder; Parkinson's disease;  
   Alzheimer's disease; amyotrophic lateral sclerosis; diabetes;  
   Huntington's disease; glioma; retinal degeneration; hearing loss;  
   gene therapy.  
KV Homo sapiens.  
OS Homo sapiens.  
PN M09740152-A1.  
PD 30-OCT-1997.  
PF 15-APR-1997; U06281.  
PR 14-APR-1997; US-837199.  
PR 22-APR-1996; US-015907.  
PR 09-MAY-1996; US-017221.  
RA (AMGC-) AMGEN INC.  
PI Fox GW, Jing S, Wen D;  
DR WPI: 97-535836/49.  
DR N-PDB: T88419.  
PT Glial cell line derived neurotrophic factor receptor - useful to  
   treat dopaminergic nerve cell disorders, e.g. Parkinson's and  
   Alzheimer's disease  
PS Claim 1: Pages 91-93; 196pp; English.  
CC The present sequence is the human glial cell line-derived  
   neurotrophic factor (GDNF) receptor, which can be used to treat  
   dopaminergic nerve cell disorders, e.g. Parkinson's and Alzheimer's  
   disease or amyotrophic lateral sclerosis, complications of diabetes  
   and Huntington's disease and (optionally in combination with GDNF)  
   glaucoma, retinal degeneration and hearing loss caused by injury to  
   inner ear sensory neurons. The receptor can also be used to block  
   unwanted GDNF activity, analyse GDNF related molecules and  
   stabilise GDNF in pharmaceutical formulations. Receptor expressing  
   cells, preferably transfected ex vivo, can be used similarly by  
   implantation, and the use of the receptor cDNA in gene therapy is
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CC also contemplated. Probes based on the cDNA can be used to identify GDNF responsive cells and tissues, e.g. to identify patients at risk who would benefit from GDNF therapy, and abnormalities in receptor expression, and to isolate molecules that form a complex with GDNF. CC cDNA or are homologous/cross-reactive with the cDNA. Anti-receptor antibodies, oligonucleotides derived from the cDNA and animal models that overexpress the receptor can be used to study the biological function of GDNF, knockout transgenic animals can be used to detect GDNF dependent neurons or processes and the antibody can be used in immunoassays for the receptor. The receptor binds GDNF specifically and with high affinity, acting as part of a complex that mediates/enhances signal transduction by GDNF, i.e. increasing dopamine uptake in dopaminergic cells.

Sequence 465 AA;

Query Match 44.9%; Score 1520; DB 28; Length 465;
Best Local Similarity 48.1%; Pred. No. 1,09e-148;
Matches 222; Conservative 101; Mismatches 122; Indels 17; Gaps 15

	DB	Accession	Score	Length	Start	End	Identical	Mismatch	Indel	Gap
D	B	F12147.1	1520	465	1	465	100%	0	0	0
O	Y	U00001.1	1520	465	1	465	100%	0	0	0
D	B	F12147.1	1520	465	1	465	100%	0	0	0
O	Y	U00001.1	1520	465	1	465	100%	0	0	0
D	B	F12147.1	1520	465	1	465	100%	0	0	0
O	Y	U00001.1	1520	465	1	465	100%	0	0	0
D	B	F12147.1	1520	465	1	465	100%	0	0	0
O	Y	U00001.1	1520	465	1	465	100%	0	0	0
D	B	F12147.1	1520	465	1	465	100%	0	0	0
O	Y	U00001.1	1520	465	1	465	100%	0	0	0
D	B	F12147.1	1520	465	1	465	100%	0	0	0
O	Y	U00001.1	1520	465	1	465	100%	0	0	0
D	B	F12147.1	1520	465	1	465	100%	0	0	0
O	Y	U00001.1	1520	465	1	465	100%	0	0	0
D	B	F12147.1	1520	465	1	465	100%	0	0	0
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O	Y	U00001.1	1520	465	1	465	100%	0	0	0
D	B	F12147.1	1520	465	1	465	100%	0	0	0
O	Y	U00001.1	1520	465	1	465	100%	0	0	0
D	B	F12147.1								

M P E R C H
(TM)

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MParch_dp protein - protein database search, using Smith-Waterman algorithm
Run on: Mon Mar 8 14:03:59 1999; Maspar time 23.85 Seconds
Tabular output not generated. 728.716 Million cell updates/sec

Title: >US-08-866-354-36
Description: (1-464) from US08866354.pep
Perfect Score: 3386
Sequence: 1 MILANVFCLFFFLDDTLRLSL.....RAPSALTYLSVLMKIAL 464

Scoring table:
PAM 150
Gap 11

Searched: 116738 segs, 37463448 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: p1r58
1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 46.701; Variance 78.241; scale 0.597

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	782	23.1	397	2 JE0082	GPI-linked receptor -	1.79e-154
2	100	3.0	452	2 S68456	translatation elongatio	1.84e-01
3	100	3.0	452	2 S62767	translatation elongatio	1.84e-01
4	103	3.0	1712	2 A38261	masking protein precu	6.65e-02
5	95	2.8	113	2 C70927	probable rps protein	9.54e-01
6	96	2.8	201	2 A47096	response regulator ho	6.90e-01
7	96	2.8	344	2 S72723	dipeptide transport p	6.90e-01
8	95	2.8	408	1 QRH0BE	Beta-3-adrenergic rec	9.54e-01
9	95	2.8	414	1 ORH0B3	Beta-3-adrenergic rec	9.54e-01
10	90	2.7	189	2 E69410	acetoin utilization p	4.62e+00
11	91	2.7	342	2 A45524	cysteine protease (3.39e+00
12	91	2.7	342	2 A45524	cysteine protease (3.39e+00
13	91	2.7	352	2 A57164	major allergen Bla g	3.39e+00
14	91	2.7	428	2 S67176	tRNA isopentenyltrans	3.39e+00
15	93	2.7	452	2 S62768	translatation elongatio	1.81e+00
16	90	2.7	568	2 S74481	probable phosphoester	4.62e+00
17	93	2.7	799	1 TVRTTB	nerve growth factor r	1.81e+00
18	91	2.7	879	1 ORRTLD	LDL receptor precursor	3.39e+00
19	92	2.7	1603	2 S17983	gene posterior sex co	2.48e+00
20	92	2.7	2410	1 JQ1948	genome polypotein 1	2.48e+00
21	92	2.7	2412	1 JQ1537	genome polypotein 1	2.48e+00
22	90	2.7	2907	2 A57278	fibrillin-2 precursor	4.62e+00
23	89	2.6	302	1 WZBE9	gene 9 protein - huma	6.27e+00

24	89	2.6	325	2 A40963	phospholipase A2-act1	6.27e+00
25	89	2.6 <td>354<td>2 B56392</td><th>beta-galactoside alph</th><th>6.27e+00</th></td>	354 <td>2 B56392</td> <th>beta-galactoside alph</th> <th>6.27e+00</th>	2 B56392	beta-galactoside alph	6.27e+00
26	88	2.6 <td>379</td> <td>2 A44473</td> <td>UTP--hexose-1-phospha</td> <td>8.50e+00</td>	379	2 A44473	UTP--hexose-1-phospha	8.50e+00
27	88	2.6 <td>379</td> <td>2 I57459</td> <td>galactose-1-phosphate</td> <td>8.50e+00</td>	379	2 I57459	galactose-1-phosphate	8.50e+00
28	88	2.6 <td>418</td> <td>2 G02953</td> <td>beta-3-adrenergic rec</td> <td>8.50e+00</td>	418	2 G02953	beta-3-adrenergic rec	8.50e+00
29	88	2.6 <td>432</td> <td>1 DEM2MC</td> <td>malate dehydrogenase</td> <td>8.50e+00</td>	432	1 DEM2MC	malate dehydrogenase	8.50e+00
30	88	2.6 <td>463</td> <td>2 A26652</td> <td>type I site-specific</td> <td>8.50e+00</td>	463	2 A26652	type I site-specific	8.50e+00
31	88	2.6 <td>480</td> <td>2 S60381</td> <td>RPD3 protein homolog</td> <td>8.50e+00</td>	480	2 S60381	RPD3 protein homolog	8.50e+00
32	87	2.6 <td>493</td> <td>2 JC5621</td> <td>epidermal growth fact</td> <td>1.15e+00</td>	493	2 JC5621	epidermal growth fact	1.15e+00
33	89	2.6 <td>503</td> <td>4 S23741</td> <td>hypothetical tPR/TRK</td> <td>6.27e+00</td>	503	4 S23741	hypothetical tPR/TRK	6.27e+00
34	88	2.6 <td>621</td> <td>2 S26691</td> <td>serine proteinase (EC</td> <td>8.50e+00</td>	621	2 S26691	serine proteinase (EC	8.50e+00
35	89	2.6 <td>700</td> <td>1 TVHUTT</td> <td>nerve growth factor I</td> <td>6.27e+00</td>	700	1 TVHUTT	nerve growth factor I	6.27e+00
36	89	2.6 <td>808</td> <td>1 VGBESM</td> <td>glycoprotein B precu</td> <td>6.27e+00</td>	808	1 VGBESM	glycoprotein B precu	6.27e+00
37	89	2.6 <td>854</td> <td>1 ORHYLD</td> <td>LDL receptor precursor</td> <td>6.27e+00</td>	854	1 ORHYLD	LDL receptor precursor	6.27e+00
38	88	2.6 <td>863</td> <td>2 S41984</td> <td>SIPI protein - yeast</td> <td>8.50e+00</td>	863	2 S41984	SIPI protein - yeast	8.50e+00
39	88	2.6 <td>925</td> <td>2 A39216</td> <td>plasma cell membrane</td> <td>8.50e+00</td>	925	2 A39216	plasma cell membrane	8.50e+00
40	87	2.6 <td>1115</td> <td>2 S64101</td> <td>PAN2 protein - yeast</td> <td>8.50e+00</td>	1115	2 S64101	PAN2 protein - yeast	8.50e+00
41	89	2.6 <td>1404</td> <td>2 A36666</td> <td>sestrate protein procu</td> <td>8.50e+00</td>	1404	2 A36666	sestrate protein procu	8.50e+00
42	89	2.6 <td>1408</td> <td>2 S16148</td> <td>gene sestrate protein</td> <td>8.50e+00</td>	1408	2 S16148	gene sestrate protein	8.50e+00
43	89	2.6 <td>2703</td> <td>2 A24420</td> <td>notch protein - frog</td> <td>8.50e+00</td>	2703	2 A24420	notch protein - frog	8.50e+00
44	88	2.6 <td>2871</td> <td>2 A55567</td> <td>fibrillin I - bovin</td> <td>8.50e+00</td>	2871	2 A55567	fibrillin I - bovin	8.50e+00
45	87	2.6 <td>2918</td> <td>2 A54105</td> <td>fibrillin-2 precursor</td> <td>8.50e+00</td>	2918	2 A54105	fibrillin-2 precursor	8.50e+00

ALIGNMENTS

RESULT	1	ALIGNMENTS
ENTRY	JE0082	#type complete
TITLE	GPI-linked receptor - mouse	
ALTERNATE_NAMES	GFRAlpha-3	
ORGANISM	#formal name Mus musculus #common name house mouse	
DATE	21-May-1998 #sequence_revision 29-May-1998 #text_channel	
	24-Sep-1998	

ACCESSIONS	JE0082
REFERENCE	JE0082
#authors	Nomoto, S.; Ito, S.; Yang, L.X.; Kiuchi, K.
#journal	Biochem. Biophys. Res. Commun. (1998) 244:849-85
#title	Molecular cloning and expression analysis of GFRalpha-3 novel cDNA related to GDNFRalpha and NTRalpha.

#accession	JE0082
#molecule-type <td>mRNA</td>	mRNA
#residues <td>1-397 #label NOM</td>	1-397 #label NOM
#cross-references <td>DBJ:AB008833; NID:q2627159; PID:q2627160</td>	DBJ:AB008833; NID:q2627159; PID:q2627160
COMMENT	This protein plays a distinct role in cell survival and differentiation.

KEYWORDS	FEATURE
1-25	
380-397	
92,145,306	

SUMMARY	#domain signal sequence #status predicted #label	#region hydrophobic\	#binding-site carbohydrate (Asn) (covalent)	#status
Query Match	23.1%	Score 782; DB 2; Length 397;		
Best Local Similarity	38.2%	Pred. No. 1.79e-154;		
Matches 123;	Conservative 78;	Mismatches 96;	Indels 25;	Gaps 18;

Db	41 CTGARKKCEANPACAKAYOHLSCTSSLRPLLESANSDCLEAEDLRNSLIDRC	100
Qy	40 CVANELCAEASNCSSRYRTLRCLAGRDRTML--ANK--ECQALLEVLOEPLVDRC	95
Db	101 HRMKHQATCLDIYVHVHPARSLGDEL-DVSYEDTV--SKPKM-NL-S-K-LN-NL	152
Qy	96 KRMRKELCQLQYVSHIGLGE-EFYEASYPEVTSRLSDIFLASIFSGTADPV	154
Db	153 KPSDCLKFAMLCTHDKDRLRKAYGACS-GI-----RCQHLCLAOIRSFEEKAAS	207
Qy	155 SAKSNHCLDAKACNLNDNCKLRSSYISICNEISPTERCNRKHKALROFDVPS	214
Db	208 HAQGLLCPAPDAGCGERRNTIAPSCALPS-VTPNCLDRSFCRADPLCRSLMDQ	266
Qy	215 YTFRMFLFCSC-QDQA-CAERRRQITLPSCSYEDKERPNCLDLAGVCRDTDLCHSLADPH	272

Dd	267	TTCGPM-DILCQPTQEOR--CLAYAGLIGTATPFIKSVNTVALS--CTCRSSGNIQ	322
Oy	273	ANCRASYQTIVTSACDAKYQCACLGSYAGMIGFDITPRITYVSSSPRGIYVSFWCSRSRGNNH	332
Dd	323	DECEQLERSEQRNPCLVEAIIAA	344
Oy	333	ECEEKFRLDFENPCLRNNAIO	354
RESULT	2		
ENTRY		S68466	#type complete
TITLE		translation elongation factor Tu-like protein P43 precursor,	
ORGANISM		mtochondrial - human	
DATE		#format_name Homo sapiens #common_name man	
ACCESSIONS		17-Jul-1998 #sequence_revision 17-Jul-1998	#text_change
REFERENCE		28-Aug-1998	
#authors		S68466; S78551; I53499	
#journal		I53499	
#title		Wells, J.; Henkier, F.; Leversha, M.; Koshy, R.	
FEBB Lett. (1995) 358:119-125		A mitochondrial elongation factor-like protein is over-expressed in tumours and differentially expressed in normal tissues.	
#accession		S68466	
#molecule_type		mRNA	
#residues		1-452 ##label WEL	
#cross-references EMBL:S75463; NID:g833998; PID:g833999			
#experimental_source liver			
#note		It is uncertain whether Met-1 or Met-4 is the initiator	
#accession		S78551	
#molecule_type		protein	
#residues		57-65;239-270;352-361 ##label WES	
GENETICS			
#gene		GDB:P43	
#cross-references GDB:G31149			
#map_position 16p12-16p11.2			
#genome		nuclear	
CLASSIFICATION		#superfamily translation elongation factor Tu; translation elongation factor Tu homology	
KEYWORDS		GTP binding; mitochondrion; P-loop	
FEATURE			
61-187		#domain translation elongation factor Tu homology [label ER]	
67-74		#region nucleotide-binding motif A (P-loop)\	
184-187		#region GTP-binding NKXD motif\	
219-221		#region GTP-binding SAK/L motif\	
73-74,110,184,185,			
187,219		#binding_site Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser)	
SUMMARY		#status Predicted	
		#length 452 #molecular_weight 49533 #checksum 1798	
Query Match		3.0%; Score 100;	DB 2; Length 452;
Best Local Similarity 27.6%; Pred. NO.1.84e-01;			
Matches 21; Conservative 19; Mismatches 31; Indels 5; Gaps 4;			
Dd	231	LGLISVKXLDADVTVYPAPDLEKFLPEAVSYSGRVGYVTGLEIILKKSDGC	290
Oy	114	LGLTEGEFFIEHA-SPIEVPYSR-LSDIFILA--SIKSGTAGDPVYSASKNH-CLEDAAKAC	168
Dd	291	ELLGHSKNRIRTYGTI	306
Oy	169	NLNNDCKKRSLRSYSI	184
RESULT	3		
ENTRY		S62767	#type complete
TITLE		translation elongation factor EF-Tu precursor - human	
ORGANISM		#format_name Homo sapiens #common_name man	
DATE		24-Aug-1996 #sequence_revision 13-Mar-1997	#text_change
ACCESSIONS		28-Aug-1998	
REFERENCE		S62767	
#authors		Morlix, V.L.; Burkhardt, W.; Spremulll, L.L.	

```

#journal      #title      #accession
#status      #molecule_type mRNA      #residues      ##cross-references EMBL:L89895; NID:g704415; PID:g704416
GENETICS
CLASSIFICATION
KEYWORDS
FEATURES
58-184      #domain translation elongation factor Tu homology
64-71      EFL\
181-184      #region nucleotide-binding motif A (P-loop)\
219-221      #region GRP-binding NKXD motif\
70,71,107,181,182, #region GRP-binding SAK/L motif\
184,219      #binding-site Mg-GTP (lys, Thr, Thr Asn, Lys, Asp)
SUMMARY      #length 452 #molecular-weight 49540 #checksum 1
Query Match      3.0%; Score 100; DB 2; Length 452;
Best Local Similarity 27.6%; Pred. No. 1,84e+01;
Matches 21; Conservative 19; Mismatches 31; Indels 5; Gaps 0;
Db 231 LGKTSVKLLDAVDTPIVPARDLEPFELPEAVSYSPGRGVTTGLRGLLK...
QY 114 LGLEGESEFEFA-SPEEPTSR-LSDIFPLA--SIFSQTGADPVYSASNN-CLDAAK...
QY 169 NLNDNCKRLRSYSTSI 184
Db 291 ELGHSKNIRTVTGI 306
QY 169 NLNDNCKRLRSYSTSI 184

RESULT 4
ENTRY      A38261      #type complete
TITLE      masking protein precursor - rat
ORGANISM   #formal_name Rattus norvegicus #common_name Norway rat
DATE       14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change 10-Sep-1997
ACCESSIONS
REFERENCE   A38261
AUTHORS    Tsurji, T.; Okada, F.; Yamaguchi, K.; Nakamura, T.
JOURNAL    Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8835-8839
TITLE      Molecular cloning of the large subunit of transforming growth factor type beta masking protein and expression of the mRNA in various rat tissues.
##cross-references MOID:910623f3
#accession A38261
#status preliminary
#molecule_type mRNA
#residues 1-1712 #label T5U
##cross-references GB:M55431; NID:g207285; PID:g207286
CLASSIFICATION #superfamily LDL receptor ligand-binding repeat homology
SUMMARY      #length 1712 #molecular_weight 165598 #checksum 9047

Query Match      3.0%; Score 103; DB 2; Length 1712;
Best Local Similarity 34.9%; Pred. No. 6,65e+02;
Matches 15; Conservative 12; Mismatches 12; Indels 4; Gaps 4;
Db 1032 DECLAP-KVCT-NGSCTNLEGSYMCXHKGYSP-T-P-DHRHQ 1070
QY 159 NHCLDAAKACNLNDNCKRLRSYSTISICNRNEISPTERCNRKCH 201

RESULT 5
ENTRY      C70927      #type complete
TITLE      probable rplis protein - Mycobacterium tuberculosis (strain H37RV)
ORGANISM   #formal_name Mycobacterium tuberculosis
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PR 08-MAY-1996: US-017427.
 PR 07-JUN-1996: US-019300.
 PR 16-JUL-1996: US-021859.
 PA (BIOJ) BIOGEN INC.
 PI Cate RL, Hession C, Sanicola-Nadel M;
 DR WPI: 98-018431/02.
 P-PSDB: W37462.
 PT New nucleic acid encoding ret receptor ligands and related proteins
 PT - vectors, transformed cells and antibodies, used for promoting cell
 PT growth and improving survival of injured cells, especially renal or
 PT nerve cells
 PS Claim 1: Page 79-80; 113pp: English.
 CC This sequence comprises a partial cDNA clone, designated g3128,
 CC for human Ret ligand (RetL) (see W37462), a key component of
 CC the Ret signaling pathway. It was isolated from a human adult
 CC heart cDNA library using a probe derived from a mouse RetL partial
 CC cDNA (see V00256). A full-length sequence (see V00251) for human
 CC RetL cDNA has also been obtained, as well as rat and human RetL,
 CC containing RetL DNA and prokaryotic or eukaryotic host cells
 CC transformed or transfected with these vectors are claimed, as well
 CC as a method for production of RetL; its soluble variants and
 CC fusion proteins with a toxin, imageable compound or radionuclide.
 CC RetL, optionally when expressed from vectors in vivo, is used to
 CC promote growth of new tissue and survival of damaged tissue,
 CC particularly kidney or neural tissue. Typical applications are in
 CC renal failure, nephritis, kidney transplants, toxic or hypoxic
 CC injury, neurodegeneration, motor neurone disease, multiple
 CC sclerosis, bacterial, viral or prion infections (e.g. meningitis,
 CC myelopathy associated with HIV or Creutzfeldt-Jakob disease),
 CC cranial nerve or spinal cord injury, developmental disorders such
 CC as Down's syndrome and cerebral palsy, or conditions involving the
 CC peripheral nervous system (Lyme disease, muscular dystrophy and
 CC amyotonia gravis). Fusion proteins are used to deliver toxins
 CC etc. to Ret-expressing cells, especially tumours.
 SQ Sequence 1271 BP: 264 A; 414 C; 316 G; 277 T;

Query Match 58.7%: Score 1169; DB 39; Length 1271;
 Best Local Similarity 99.7%: Pred. No. 0.00e+00;
 Matches 1172; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

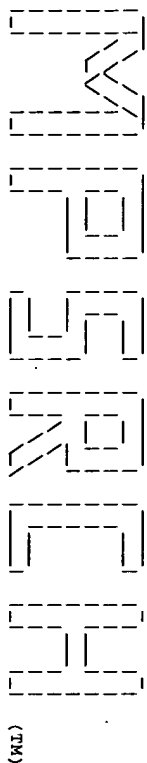
DB 15 caccctcaactagaagaacagctctctgataagctgcatgctgacacggcgatgaagaac 74
 QY 471 CACAGCAACTCAGGAAACGCTCTCGATGAGCTGATGCTGACCGCGCATGAAGAAC 530
 DB 75 aggttgctctgttgacactctatgtgacagcttaacagctgcccgaagccttgtaactgt 134
 QY 531 AGGTTGCTGCTTGACATCTATTGGACCGTTACCGGCGCAGCCTTGTAATATG 590
 DB 135 agctgagatgtctcccccataagaacacagctgacacgaacacccctgtgaataatccta 194
 QY 591 AGCTGAGATGTCCTCCCTATGAAGACACAGTACAGCAAAACCTCGAAATGATCTCA 650
 DB 195 gcaaaactgaacatgctcaaacacagactcagacccctctgacaggttgcatgtgtgta 254
 QY 651 GCAAACTGAACATGCTCAAAACAGACTCAGACCTCTGCTCAAGTTGCCATGCTGTA 710
 DB 255 ctctcaatagaagaatgtgacagctgctgccaagagcctaagaggagagcgctgcccggccc 314
 QY 711 CTCTCAATGACAAAGTGTACCGGCTGCCCAAGGCTTAGGGGAGGCGTCTCCGGCCCC 770
 DB 315 actgcagacgacagctgctcctcagagcagctgactactttctgagaagcgccggagc 374
 QY 771 ACTGCACAGCGCAGCTGCTGCTCAGGACGCTGCTACTTCTTGAGAGAGCCGCCACAC 830
 DB 375 ccaacgagcagggcctgctactgtgccatgtgcccccaacgaacccgggctgcgggagac 434
 QY 831 CCCACGCGCAGGCGCTGCTACTGTGCCCATGTGCCCAAGACCGGCGGCTGCGGGAGAC 890
 DB 435 gcggcggaagaacacacgcccccaactgcgcgctgacggcgctgagcccccaactgctgg 494
 QY 891 GCCGCGGACACCATCTCCGCCCAACTGCGGCTGCCCGCTGTGGCCCCCAACTGCTGG 950

DB 495 agctgcggcgacctctgtctctccgacccgcttgacagatcacgccttggatccaga 554
 QY 951 AGCTGCGGCGCCTGCTGCTCTCCGACCCGCTTGACATCAGCGCTGTGATCTTCACA 1111
 DB 555 cccactgcacatccatgagacatccctagaaactgtgtcaacagagcagctccagatgt 1171
 QY 1011 CCCACTGCATCCCATGATCCATGAGATCCTAGAACTGTGTGACAGAGCACTCCAGATG 1171
 DB 615 gagacatccggggctgattgtgagctgcataagcccccaacttgtaagcaatgtgtgt 1231
 QY 1071 GAGCATACCTGGGCTGATTTGGACTGCTGACCTGACCCCAACTTGGCCAGCAATGTA 1231
 DB 675 ccaagtgtgcttaagtacactgacacccgagcaggtgtgcaacccctgacagagagagag 1291
 QY 1131 CCAATGTGCTTATAGTGCACGTCGCGAGGAGTGCACACCTGACAGAGAGATGTGTA 1291
 DB 735 tgcctggaagggtctctctcccaacaacccctgctctacagagagcattgacatgac 1351
 QY 1191 TGCTGGAAGGTTCTTCTCCACACACCCCTGCTCAGAGAGCCATGACAGTAAATGTC 1351
 DB 795 gtttcaacgacacactctctccagagactggccacacccctactgtgctgagatgtac 1411
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 DB 855 accagaaatgaaaacccctgctgtgagggcacaagccctgtgtgctctctctctctct 1471
 QY 1311 ACCGAATGAAGAACCCGCTGATGAGGCGACAGCCCTGGGCTCTTCTTCTCCAGTA 1471
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 DB 1035 aaggaggtgacagtcagacagatgagggcacagagaaactaagggttataagcctccaaac 1651
 QY 1491 AAGAGAGTGCAGTGCAGATGAGAGGCGACAGAGAACTAAGGTTATGACTCCACATC 1651
 DB 1095 ctacatgctcagctcctcctcctccacccatccctcactctgatactatgctgcct 1711
 QY 1551 CTTACTGTCAGTCCATCTCTCTCCACCCCATCTCCACTTGATTCATGCTGCCCT 1711
 DB 1155 ccttggtgacacatctagcatgtcatgtgtg 1189
 QY 1611 CTTGTGTCACCAATTTAGCATGATCTGTG 1645

RESULT 3
 ID V00249 standard: cDNA; 1889 BP.
 AC V00249, 1997.
 DT 21-MAY-1998 (first entry)
 DE Mouse Ret ligand RetL3 cDNA.
 KW Ret ligand; RetL; RetL3; receptor; signal transduction; mouse;
 KW cell growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury;
 KW neurodegeneration; motor neurone disease; multiple sclerosis;
 KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
 KW cranial nerve injury; spinal cord injury; Down's syndrome;
 KW amyotonia gravis; tumour; therapy; ss.
 OS Mus musculus.
 FH Key location/Qualifiers
 FT CDS 41..1234
 FT /tag- a
 PN MO9744356-A2.
 PD 27-NOV-1997.
 PE 07-MAY-1997: 007726.
 PR 10-APR-1997: US-017427.
 PR 08-MAY-1996: US-017427.
 PR 07-JUN-1996: US-019300.
 PR 16-JUL-1996: US-021859.

PT New nucleic acid encoding ret receptor ligands and related proteins
PT - vectors, transformed cells and antibodies, used for promoting cell
PT growth and improving survival of injured cells, especially renal or
PT nerve cells
PS Claim 1: Page 79-80; 113pp: English.
CC This sequence comprises a partial cDNA clone, designated GJ128,
CC for human Ret ligand (RetL3 (see W37462)), a key component of
CC the Ret signalling pathway. It was isolated from a human adult
CC heart cDNA library using a probe derived from a mouse RetL3 partial
CC cDNA (see V00256). A full-length sequence (see V00251) for human
CC RetL3 cDNA has also been obtained, as well as rat and human RetL1,
CC human RetL2 and mouse RetL3 sequences (see V00245-51). Vectors
CC containing RetL3 DNA and prokaryotic or eukaryotic host cells
CC transformed or transfected with these vectors are claimed, as well
CC as a method for production of RetL3, its soluble variants and
CC fusion proteins with a toxin, imageable compound or radionuclide.
CC RetL3, optionally when expressed from vectors in vivo, is used to
CC promote growth of new tissue and survival of damaged tissue,
CC particularly kidney or neural tissue. Typical applications are in
CC renal failure, nephritis, kidney transplants, toxic or hypoxic
CC injury, neurodegeneration, motor neurone disease, multiple
CC sclerosis, bacterial, viral or prion infections (e.g. meningitis,
CC myelopathy associated with HIV or Creutzfeldt-Jakob disease),
CC cranial nerve or spinal cord injury, developmental disorders such
CC as Down's syndrome and cerebral palsy, or conditions involving the
CC peripheral nervous system (Lyme disease, muscular dystrophy and
CC myasthenia gravis). Fusion proteins are used to deliver toxins
CC etc. to Ret-expressing cells, especially tumours.
SQ Sequence 1271 BP; 264 A; 414 C; 316 G; 277 T;
Query Match 4.1%; Score 81; DB 39; Length 1271;
Best Local Similarity 98.8%; Pred. No. 5,61e-33;
Matches 82; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 1184 ctggcctgtggcctgtgtatctctatctgtcctaagctctcgtgctctg 1243
Cp 84 CTGGAGCCTGTGGCCTGTGTATCTCTATTTATGCTCTAAAGCTCTGGGCTCTG 25
Db 1244 gatacagataaaccttgacct 1266
Cp 24 GATCATGATTAACCTTGACTT 2
RESULT 6
ID V00251 standard; cDNA; 1699 BP.
AC V00251;
DT 21-MAY-1998 (first entry)
DE Human Ret ligand RetL3 cDNA.
KW Ret ligand; RetL; RetL3; receptor; signal transduction; human;
KW cell growth; renal cell; nerve cell; renal failure; nephritis;
KW kidney transplant; toxic injury; hypoxic injury;
KW neurodegeneration; motor neurone disease; multiple sclerosis;
KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
KW cranial nerve injury; spinal cord injury; Down's syndrome;
KW cerebral palsy; Lyme disease; muscular dystrophy;
KW myasthenia gravis; tumour; therapy; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 175..1377
FT /tag- a
FN WO9744356-A2.
PD 27-NOV-1997.
PF 07-MAY-1997; 007726.
PR 10-APR-1997; US-017427.
PR 08-MAY-1996; US-017427.
PR 07-JUN-1996; US-019300.
PR 16-JUL-1996; US-021859.
PA (BIOJ) BIOGEN INC.
PI Cate RL, Hession C, Sanicola-Nadel M;
DR WPI: 98-018431/02.
P-PSDB: W37463.
PT New nucleic acid encoding ret receptor ligands and related proteins
PT - vectors, transformed cells and antibodies, used for promoting cell

PT growth and improving survival of injured cells, especially renal or
PT nerve cells
PS Claim 1: Page 82-84; 113pp: English.
CC This sequence comprises cDNA encoding human Ret ligand (RetL3 (see
CC (see W37463)), a key component of the Ret signalling pathway. It is
CC a composite of partial clone GJ148 (see V00250), obtained from an
CC adult heart cDNA library, and of clone GJ135, isolated from an
CC adult spinal cord cDNA library. Rat and human RetL1, human RetL2
CC and mouse RetL3 sequences are also claimed (see W37457-62). Vectors
CC containing RetL3 DNA and prokaryotic or eukaryotic host cells
CC transformed or transfected with these vectors are claimed, as well
CC as a method for production of RetL3, its soluble variants and
CC fusion proteins with a toxin, imageable compound or radionuclide.
CC RetL3, optionally when expressed from vectors in vivo, is used to
CC promote growth of new tissue and survival of damaged tissue,
CC particularly kidney or neural tissue. Typical applications are in
CC renal failure, nephritis, kidney transplants, toxic or hypoxic
CC injury, neurodegeneration, motor neurone disease, multiple
CC sclerosis, bacterial, viral or prion infections (e.g. meningitis,
CC myelopathy associated with HIV or Creutzfeldt-Jakob disease),
CC cranial nerve or spinal cord injury, developmental disorders such
CC as Down's syndrome and cerebral palsy, or conditions involving the
CC peripheral nervous system (Lyme disease, muscular dystrophy and
CC myasthenia gravis). Fusion proteins are used to deliver toxins
CC etc. to Ret-expressing cells, especially tumours.
SQ Sequence 1699 BP; 328 A; 562 C; 468 G; 341 T;
Query Match 4.1%; Score 81; DB 39; Length 1699;
Best Local Similarity 98.8%; Pred. No. 5,61e-33;
Matches 82; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 1612 ctggcctgtggcctgtgtatctctatctgtcctaagctctcgtgctctg 1671
Cp 84 CTGGAGCCTGTGGCCTGTGTATCTCTATTTATGCTCTAAAGCTCTGGGCTCTG 25
Db 1672 gatacagataaaccttgacct 1694
Cp 24 GATCATGATTAACCTTGACTT 2
RESULT 7
ID V00256 standard; cDNA; 1878 BP.
AC V00256;
DT 21-MAY-1998 (first entry)
DE Mouse Ret ligand RetL3 cDNA partial clone (ESR AA50083).
KW Ret ligand; RetL; RetL3; receptor; signal transduction; mouse;
KW cell growth; renal cell; nerve cell; renal failure; nephritis;
KW kidney transplant; toxic injury; hypoxic injury;
KW neurodegeneration; motor neurone disease; multiple sclerosis;
KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
KW cranial nerve injury; spinal cord injury; Down's syndrome;
KW cerebral palsy; Lyme disease; muscular dystrophy;
KW myasthenia gravis; tumour; therapy; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT CDS 205..1245
FT /tag- a
FN WO9744356-A2.
PD 27-NOV-1997.
PF 07-MAY-1997; 007726.
PR 10-APR-1997; US-017427.
PR 08-MAY-1996; US-017427.
PR 07-JUN-1996; US-019300.
PR 16-JUL-1996; US-021859.
PA (BIOJ) BIOGEN INC.
PI Cate RL, Hession C, Sanicola-Nadel M;
DR WPI: 98-018431/02.
P-PSDB: W37465.
PT New nucleic acid encoding ret receptor ligands and related proteins
PT - vectors, transformed cells and antibodies, used for promoting cell
PT growth and improving survival of injured cells, especially renal or
PT nerve cells
PS Disclosure; Page 71-73; 113pp: English.



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MParch_n n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Fri Mar 12 03:17:56 1999; MParch time 2882.03 Seconds
Tabular output not generated. 1237.127 Million cell updates/sec

Title: >US-08-866-354-37
Description: (1-1991) from US08866354.seq
Perfect Score: 1991
N.A. Sequence: 1 CAAGTCAGGTTTATCATG.....CATGATTAACCTTGACG 1991
Comp: GTTCAGTTTCCAAATTAATGTA.....GTACTAATTTGGAACTGAC

Scoring table: TABLE default
Gap 6

Mmatch STD : Dbase 0; Query 0

Searched: 2275026 seqs, 895388244 bases x 2

Post-processing: Minimum match 0%

Listing first 45 summaries

Database: emb1-est56
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genbank-est109
5:gb_est1 6:gb_est10 7:gb_est11 8:gb_est12 9:gb_est13
10:gb_est14 11:gb_est15 12:gb_est16 13:gb_est17
14:gb_est18 15:gb_est19 16:gb_est2 17:gb_est20
18:gb_est21 19:gb_est3 20:gb_est4 21:gb_est5 22:gb_est6
23:gb_est7 24:gb_est8 25:gb_est9 26:gb_gss1 27:gb_gss2
28:gb_gss3 29:gb_gss4

Statistics: Mean 11.743; Variance 2.290; scale 5.129

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
C 1	454	22.8	474	11	AA694259	z13id11.s1 Soares feta 0.00e+00
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C 3	389	19.5	396	11	AA687725	nv08c06.s1 NCI_CGAP.Pr 0.00e+00
C 4	358	18.0	373	11	AA676356	z159g01.s1 Soares feta 0.00e+00
C 5	352	17.7	436	21	W69813	z4d8g06.s1 Soares feta 0.00e+00
C 6	332	16.7	350	15	AA694036	oq02f02.s1 NCI_CGAP.Lu 0.00e+00
C 7	289	14.5	442	22	AA049894	mj1id08.s1 Soares feta 0.00e+00
C 8	232	11.7	465	21	AA050083	mj08d05.s1 Soares feta 0.00e+00
C 9	181	9.1	373	11	AA676356	z139h12.s1 Soares feta 0.00e+00
C 10	160	8.0	373	11	AA676356	z139h12.s1 Soares feta 0.00e+00
C 11	160	8.0	396	11	AA687725	nv08c06.s1 NCI_CGAP.Pr 0.00e+00
C 12	160	8.0	474	11	AA694259	z13id11.s1 Soares feta 0.00e+00
C 13	158	7.9	350	15	AA694036	oq02f02.s1 NCI_CGAP.Lu 0.00e+00

14	158	7.9	450	21	W69774	z4d8g06.s1 Soares feta 0.00e+00
15	152	7.6	353	21	AA041935	mj04d08.s1 Soares feta 0.00e+00
16	140	7.0	502	23	AA238748	my35d09.s1 Soares feta 0.00e+00
17	63	3.2	222	12	AA754459	97SN1787 Rice Immature 2.52e-10
18	63	3.2	252	12	AA754459	97SN1787 Rice Immature 2.52e-10
19	53	2.7	436	21	W69813	z4d8g06.s1 Soares feta 0.00e+00
20	48	2.4	247	12	AA754458	97SN1784 Rice Immature 2.52e-10
21	45	2.3	247	12	AA754458	97SN1784 Rice Immature 2.52e-10
22	39	2.0	478	21	W73581	z455h01.s1 Soares feta 0.00e+00
23	37	1.9	350	25	AA349976	EST35965 Infant brain 1.09e-11
24	34	1.7	189	11	AA676213	z139h12.s1 Soares feta 0.00e+00
25	33	1.7	431	18	AA179473	EST223187 Normalized r 2.52e-10
26	33	1.7	499	14	AA925330	UT-R-AI-ek-h-10-0-UI.s 6.00e-11
27	32	1.6	355	21	HS278350	H.sapiens mRNA, expres 4.41e-11
28	31	1.6	415	17	AT073842	oc01h09.s1 Soares feta 4.41e-11
29	31	1.6	419	20	HSDBEC059	H.sapiens partial cDN 4.41e-11
30	31	1.6	607	26	B16636	342P20.TPB C17978SKAI 4.41e-11
31	31	1.6	650	20	W27487	3194 Human retina cDNA 4.41e-11
32	32	1.6	2275	11	AF034173	Homo sapiens ntcon2 co 1.09e-11
33	30	1.5	255	20	W46820	EST112821 Embryo, 8 we 2.52e-10
34	29	1.5	225	24	AA287263	0556g10.s1 NCI_CGAP.GC 2.52e-10
35	29	1.5	308	14	AA894529	EST15382 Retina II Hom 2.52e-10
36	29	1.5	321	24	AA317449	0236c11.x1 Soares feta 2.52e-10
37	29	1.5	396	17	AT080124	EST223292 Normalized r 2.52e-10
38	29	1.5	448	18	AA180186	y775d11.s1 Homo sapien 2.52e-10
39	29	1.5	448	19	N58868	z189h09.s1 Soares feta 2.52e-10
40	29	1.5	467	11	AA705382	UT-R-AI-ek-h-10-0-UI.s 1.09e-11
41	29	1.5	459	14	AA925330	Homo sapiens mRNA; exp 1.09e-11
42	30	1.5	502	9	HS298510	ue96g10.Y1 Susano mus 2.52e-10
43	30	1.5	535	17	AA115975	F.rubripes GSS sequenc 2.52e-10
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ALIGNMENTS

RESULT 1 AA694259 474 bp mRNA EST 16-DEC-1997
LOCUS z13id11.s1 Soares feta liver spleen INFUS S1 Homo sapiens cDNA
DEFINITION Clone 432405 3', mRNA sequence.
ACCESSION AA694259
NID 92695197
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 474)

REFERENCE Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisels, G., Jost, S.,
Kritzman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
Martin, J., Moore, B., Schellenberg, K., Stepien, M., Tan, F.,
Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-NCI human EST Project
Unpublished (1997)

TITLE

JOURNAL

COMMENT

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LNL: contact lnl@imaseconsortium.org (info@imaseconsortium.gov) for further information.
Seq primer: -40m3 fwd. ET from Amerisham
High quality sequence stop: 451.
Location/Qualifiers
1..474
/organism="Homo sapiens"
/note="Organ: Liver and Spleen; Vector: p77"
with a modified polylinker; Site 1: Pac 1
This is a subtracted version of the original
liver spleen INFUS library. 1st strand cDNA
with a Pac I - oligo(dT) primer [5'

ACTGGAAGATTAATTAAGATCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pTZ3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo."
/db_xref="GDB:1332174"
/db_xref="taxon:9606"
/clone="432405"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
BASE COUNT 134 a 100 c 137 g 103 t
ORIGIN

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Best Local Similarity 99.0% Pred. No. 0.00e+00;
Matches 456; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Cp 1990 AGTCAAGGTTTATCATGATCCCAAGAGCCAGAGACTTTAGACATTAATAGGAATA 1931
Db 77 AAGCAAGGCCACAGGCTCCAGCTCTGATGCCAGATGTCGCGAGATCCGGGACAG 136
|||||
Cp 1930 AAGCAAGGCCACAGGCTCCAGCTCTGATGCCAGATGTCGCGAGATCCGGGACAG 1871
Db 137 GGCAGTGCAGGAGTAGTTTCCATCTCCACTCAGAGAGAGAGAGAGAGAGAGAGAG 196
|||||
Cp 1870 GGCAGTGCAGGAGTAGTTTCCATCTCCACTCAGAGAGAGAGAGAGAGAGAGAGAG 1811
Db 197 CTTCCTCACAAGAGAGATGACTTTCTAGAGTGCCTCAGAACACCAGTCTCCCTACCC 256
|||||
Cp 1810 CTTCCTCACAAGAGAGATGACTTTCTAGAGTGCCTCAGAACACCAGTCTCCCTACCC 1751
Db 257 TAACCTTAATCTGGAATGCAATAGAGATGCTTAATTAATTAATCTGATCTGTGT 316
|||||
Cp 1750 TAACCTTAATCTGGAATGCAATAGAGATGCTTAATTAATTAATCTGATCTGTGT 1691
Db 317 ACTCAAGAGAGAGGCTCTGAGAGAGGCTGTGGAGCTGCTCACCACAGATGACATGG 376
|||||
Cp 1690 ACTCAAGAGAGAGGCTCTGAGAGAGGCTGTGGAGCTGCTCACCACAGATGACATGG 1631
Db 377 CTAATATTGTGGCCACCAAGAGAGGCGAGCATGATCAGAAGTGGAGATGGGTGAGGGA 436
|||||
Cp 1630 CTAATATTGTGGCCACCAAGAGAGGCGAGCATGATCAGAAGTGGAGATGGGTGAGGGA 1571
Db 437 ATGAGACTGACCAAGTAAAGATCTGGAGGTGATTAAC 474
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Cp 1570 ATGAGACTGACCAAGTAAAGATCTGGAGGTGATTAAC 1533

RESULT 2
LOCUS W69774 450 bp mRNA EST 16-OCT-1996
DEFINITION z48906.s1 Soares fetal heart NBH19W Homo sapiens cDNA clone
ACCESSION W69774
NID g1379032
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Eukaryotes; Chordata; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 450)
REFERENCE 1 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holtman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marz, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevisan, E., Waterston, R., Williamson, A., Wohldmann, P. and
Wilson, R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LNL : contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert length: 580 Std Error: 0.00
Seq primer: mob. REGA+ER
High quality sequence stop: 380.
Location/Qualifiers
1. 450
/organism="Homo sapiens"
/note="Organ: heart; Vector: pTZ3D (Pharmacia)";
modified polylinker; Site.1: Not I; Site.2: Eco RI;
strand cDNA was primed with a Not I - oligo(dT) primer;
TGTTACCAATCTGAGTGGGAGGCGCCGACATCTTTTCTTTTCTTTT 3';
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pTZ3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M. Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NBH19W."

BASE COUNT 130 a 96 c 134 g 87 t 3 others
ORIGIN
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Best Local Similarity 98.7% Pred. No. 0.00e+00;
Matches 442; Conservative 0; Mismatches 4; Indels 2; Gaps 2;
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Cp 1990 AGTCAAGGTTTATCATGATCCCAAGAGCCAGAGACTTTAGACATTAATAGGAATA 1931
Db 63 AAGCAAGGCCACAGGCTCCAGCTCTGATGCCAGATGTCGCGAGATCCGGGACAG 122
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Cp 1930 AAGCAAGGCCACAGGCTCCAGCTCTGATGCCAGATGTCGCGAGATCCGGGACAG 1871
Db 123 GGCAGTGCAGGAGTAGTTTCCATCTCCACTCAGAGAGAGAGAGAGAGAGAGAGAG 182
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Cp 1870 GGCAGTGCAGGAGTAGTTTCCATCTCCACTCAGAGAGAGAGAGAGAGAGAGAGAG 1811
Db 183 -TTCTCACAAGAGAGATGACTTTCTAGAGTGCCTCAGAACACCAGTCTCCCTACCC 241
|||||
Cp 1810 CTTCCTCACAAGAGAGATGACTTTCTAGAGTGCCTCAGAACACCAGTCTCCCTACCC 1751
Db 242 TAACCTTAATCTGGAATGCAATAGAGATGCTTAATTAATTAATCTGATCTGTGT 301
|||||
Cp 1750 TAACCTTAATCTGGAATGCAATAGAGATGCTTAATTAATTAATCTGATCTGTGT 1691
Db 302 AGTCAAGAGAGAGGCTCTGAGAGAGGCTGTGGAGCTGCTCACCACAGATGACATG 361
|||||
Cp 1690 AGTCAAGAGAGAGGCTCTGAGAGAGGCTGTGGAGCTGCTCACCACAGATGACATG 1631
Db 362 GCTAATATTGTGGCCACCAAGAGAGGCGAGCATGATCAGAAGTGGAGATGGGTGAGGGA 421
|||||
Cp 1631 GCTAATATTGTGGCCACCAAGAGAGGCGAGCATGATCAGAAGTGGAGATGGGTGAGGGA 1571
Db 422 AATGAGACTGACCAAGTAAAGATCTGG 449
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Cp 1571 AATGAGACTGACCAAGTAAAGATCTGG 1544

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LOCUS		nv08c06.i1	NCI-CGAP_P122	Homo sapiens	CDNA clone	IMAGE:1219594,
DEFINITION		AA687725		mrna sequence.		
ACCESSION		AA687725				
NID		92674631				
KEYWORDS		EST.				
SOURCE		human.				
ORGANISM		Homo sapiens				
REFERENCE		Eukaryote; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;				
AUTHORS		Primates; Catarrhini; Homnidae; Homo.				
TITLE		1 (bases 1 to 396)				
JOURNAL		NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .				
COMMENT		National Cancer Institute, Cancer Genome Anatomy Project (CGAP),				
		Tumor Gene Index				
		Unpublished (1997)				
		Contact: Robert Streusberg, Ph.D.				
		Tel: (301) 496-1550				
		Email: Robert_Streusberg@nih.gov				
		Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.				
		Emmert-Buck, M.D., Ph.D.				
		CDNA Library Preparation: M. Bento Soares, Ph.D.				
		CDNA Library Arrayed by: Greg Lennon, Ph.D.				
		DNA sequencing by: Washington University Genome Sequencing Center				
		clone distribution: NCI-CGAP clone distribution information can be				
		found through the I.M.A.G.E. Consortium/BLNI at:				
		www.bio.11n1.gov/dbp/1mage/1mage.html				
FEATURES		Seq primer: -40ml3 fwd. Err from Amer sham				
SOURCE		High quality sequence stop: 331.				
		Location/Qualifiers				
		1..396				
		/organism="Homo sapiens"				
		/note="Organ: prostate; Vector: pT73D-Pac (Pharmacia)				
		with a modified polylinker; 1st strand cDNA was prepared				
		from normal prostate bulk tissue, and was then primed with				
		a Not I - oligo(dT) primer. Double-stranded cDNA was				
		ligated to Eco RI adaptors (Pharmacia), digested with Not				
		I and cloned into the Not I and Eco RI sites of the				
		modified pT73 vector. Library is normalized, and was				
		constructed by Bento Soares and M. Fatima Bonaldo."				
		/db_xref="taxon:9606"				
		/clone="IMAGE:1219594"				
		/clone_11b="NCI-CGAP_P122"				
		/sex="male"				
		/tissue_type="normal prostate"				
		/lab_host="DH10B"				
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ORIGIN						
Query Match		19.5%; Score 389; DB 11; Length 396;				
Best Local Similarity		99.2%; Pred. No. 0.00e+00;				
Matches 392; Conservative		0; Mismatches 3; Indels 0; Gaps 0;				
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Db	62	AAGCAAGGCCACAGAGCTCCAGCTCTGATGCGCCAGATGTTGCGAGGATCCGGGGACAG	121			
Cp	1930	AAGCAAGGCCACAGAGCTCCAGCTCTGATGCGCCAGATGTTGCGAGGATCCGGGGACAG	1871			
Db	122	GCGAGTGCAGGACAGTAGTTTTCATCTCTCCACTCAGAGAGAGAGACGAGGGGCGAGAGC	181			
Cp	1870	GCGAGTGCAGGACAGTAGTTTTCATCTCTCCACTCAGAGAGAGAGACGAGGGGCGAGAGC	1811			
Db	182	ATTCTTCAACAAGAGATGACTTCTTGAGGCTCGCTCGAAGACACCCAGCTCCCTTACC	241			
Cp	1810	CTTCTTCAACAAGAGATGACTTCTTGAGGCTCGCTCGAAGACACCCAGCTCCCTTACC	1751			
Db	242	TAAACCTATCTGGAATGCAATGAGAAATGGCTAATTAATGATTCGTGTGATCTGT	301			

Cp	1750	TAAACCTAATTCGAGATCCATTAAGAAGGCTTAACCTATTAGATTTCTGGTGAATCCTTGCT	1691
Db	302	AGTCAAGAGGAAGGGCTCAGAAAGGGCGTTGTGGAGCTGTCACACACAGATGACATGG	361
Cp	1690	AGTCAGAGGAAGGGCTCACAAAGGGCGTTGTGGAGCTGTCACACACAGATGACATGG	1691
Db	362	CTAATTTGTGGCCACCAAGAGGGGCACAGCAT	396
Cp	1630	CTAATTTGTGGCCACCAAGAGGGGCACAGCAT	1596
RESULT	4		
LOCUS	AA678356	373 bp	mRNA EST 19-DEC-1997
DEFINITION	z125901.s1 Soares fetal liver spleen INFILS S1 Homo sapiens CDNA		
ACCESSION	AA678356		
NID	92658878		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryote; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
AUTHORS	1 (bases 1 to 373) Hillier,L., Allen,M., Bowles,L., Dubnue,T., Getzel,G., Jost,N., Kitzman,D., Kucaba,T., Lacey,M., Le,N., Lennon,G., Marra,N., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Treisman,B., White,Y., Wyllie,T., Waterston,R. and Wilson.R. Mashu-NCI human EST Project Unpublished (1997)		
TITLE			
JOURNAL			
COMMENT	Contact: Wilson RK Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.edu This clone is available royalty-free through LNL : contact@lnl.org IMAGE Consortium (info@image.lnl.gov) for further information. Seq primer: -40m13 fwd. Ex from Amersham High quality sequence stop: 365. Location/Qualifiers 1. 373 /organism="Homo sapiens" /note="Organ: Liver and Spleen; Vector: pTZ19D (Pharmacia); with a modified polylinker; Site_1: Pac I; Site_2: EcoRI; This is a subtracted version of the original SMART library. Liver spleen INFILS library. 1st strand cDNA was PCR amplified with a Pac I - oligo(dt) primer [5'] AAGTCAGAGGAATTAATTAAGAGCTTTTTTTTTTTTTTTTTTTTTTTTTTTT double-stranded cDNA was ligated to Eco RI sites (see above). (Pharmacia), digested with Pac I and cloned into pTZ19D and Eco RI sites of the modified pTZ19D vector. went through one round of normalization. Library constructed by Bento Soares and M.Felima Bonaldi. /db_xref="taxon:9606" /clone="431856" /clone_id="Soares fetal liver spleen INFILS S1" /sex="male" /dev_stage="20 week-post conception fetus" /lab_host="DH10B (ampicillin resistant)"		
BASE COUNT	107 a	107 g	80 t
ORIGIN	85 c	101 g	80 t
Query Match	18.0%	Score 358:	DB 11: Length 373:
Best Local Similarity	99.2%:	Pred. No. 0.00e+00:	Mismatches 2: Indels 1: Gaps 1:
Matches	366:	Conservative	0;
Db	6	AGTCAAGGCTTATTCATGATCCAAAGGCCAGAGAGACTTAGACATAATAGATA	65
Cp	1990	AGTCAAGGCTTATTCATGATCCAAAGGCCAGAGAGACTTAGACATAATAGATA	1991
Db	66	AAGCAAGGCCACAGAGGCTCCAGCTCTGATGCCCCAGATGTTCCGCCAGAGATCCGGGACAG	125


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CP 1930 AAGCAAGGCCACAGGCTCCAGCTCTGATGCCAGATGTCGCGAGATCCGGGACAG 1871
DB 126 GGCAGTCAGGCACTAGTTTCCATCTCCACTCAGAGGAGACAGGGGCGAGAGC 185
CP 1870 GGCAGTCAGGCACTAGTTTCCATCTCCACTCAGAGGAGACAGGGGCGAGAGC 1811
DB 186 -TTCTTCACAAGAGATGACTTCTAGGCTGCTCAGAACACCAGCTCCCTACCC 244
CP 1810 CTTTTCACAAGAGATGACTTCTAGGCTGCTCAGAACACCAGCTCCCTACCC 1751
DB 245 TAACCTTAATCTGGAATGCAATAGAGATGCTTAATTAATTTGTTGATCTGCT 304
CP 1750 TAACCTTAATCTGGAATGCAATAGAGATGCTTAATTAATTTGTTGATCTGCT 1691
DB 305 AGTCAAGGAGAGGCTCAGAAAGGGCTTGTGAGCTGCTCACCACCATGATGACATG 364
CP 1690 AGTCAAGGAGAGGCTCAGAAAGGGCTTGTGAGCTGCTCACCACCATGATGACATG 1631
DB 365 CTAATTTGT 373
CP 1630 CTAATTTGT 1622

RESULT 5
LOCUS W69813 436 bp mRNA EST 16-OCT-1996
DEFINITION z44806.r1 Soares fetal heart NBH19W Homo sapiens cDNA clone
343930 5', mRNA sequence.
ACCESSION W69813
NID 91379141
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryote; mitochondria; eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Carnivora; Homnidae; Homo.
1 (bases 1 to 436)
Haller, J., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Ma, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevisan, E., Waterston, R., Williamson, A., Wollmann, P. and
Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)

TITLE
JOURNAL
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 580 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 327.
Location/Qualifiers
1. 436
/organism="Homo sapiens"
/note="Organ: heart; Vector: pT73D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer (5'
TGTACCAATCTGGAATGCAATAGAGATGCTTAATTAATTTGTTGATCTGCT
3'),
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M. Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NBH19W."
/db_xref="taxon:9606"
/clone="343930"

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/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
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BASE COUNT 88 a 130 c 104 g 113 t 1 others
ORIGIN
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Best Local Similarity 98.0%; Pred. No. 0.00e+00;
Matches 384; Conservative 0; Mismatches 3; Indels 5; Gaps 5;

DB 41 GGAGAACTTAAGGATTATGACCTCAGATCTTATGCTGCTCCTATCCCTCCACC 100
OY 1521 GGAGAACTTAAGGATTATGACCTCAGATCTTATGCTGCTCCTATCCCTCCACC 1580
DB 101 CCATCTCCATCTTCTGATTCATGCTGCCCTCCTTGGTGGCCAAATTTAGCATGTCATC 160
OY 1581 CCATCTCCATCTTCTGATTCATGCTGCCCTCCTTGGTGGCCAAATTTAGCATGTCATC 1640
DB 161 TGGTGTGACACCTCCACCAAGCCCTTCTGAGCCCTTCTCTGACTACAGATCA 220
OY 1641 TGGTGTGACACCTCCACCAAGCCCTTCTGAGCCCTTCTCTGACTACAGATCA 1700
DB 221 CCAGATCTAATTAAGTTAGCTTCTCTATTCATTCACATTTAGGTTAGGTTAGGAG 280
OY 1701 CCAGATCTAATTAAGTTAGCTTCTCTATTCATTCACATTTAGGTTAGGTTAGGAG 1760
DB 281 GACTGGTGTCTGAGGACACCTTAGAAAGCATCTTCCTTTGGAAGAAAGCTCCGCC 340
OY 1761 GACTGGTGTCTGAGGACACCTTAGAAAGCATCTTCCTTTGGAAGAAAGCTCCGCC 1420
DB 341 CTCCTGCTCTCTCTCTCTTAAAGTGGAGATGAAACAACTGCTGCTGCTGCTGCTG 440
OY 1821 CTCCTGCTCTCTCTCTCTTAAAGTGGAGATGAAACAACTGCTGCTGCTGCTGCTG 440
DB 401 CCGGATCTCTCCGAAACATCTGGGGCATCAGA 432
OY 1877 CCGGATCTCTCCGAAACATCTGGGGCATCAGA 1907

RESULT 6
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DEFINITION OQ02F02.s1 NCI-CGAP_Lus Homo sapiens cDNA clone IMAGE:1546
ACCESSION AA984036
NID 93162561
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Carnivora; Homnidae; Homo.
1 (bases 1 to 350)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (1997)
Unpublished (1997)

TITLE
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher Moskeluk, M.D., Ph.D., NIH
Emmett-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 762 Std Error: 0.00
Seq primer: -40m13 fwd, ET from Amersham
High quality sequence stop: 284.

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FEATURES

Location/Qualifiers
1..350

/organism="Homo sapiens"
/note="Organ: lung; Vector: p773D-Pac (Pharmacia) with a modified polylinker. 1st strand cDNA was prepared from a neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."
/db_xref="taxon:9606"
/clone_1lb="NCI-CGAP_Lu5"
/tissue_type="carcinoid"
/lab_host="DH10B"

BASE COUNT

100 a 81 c 96 g 73 t

ORIGIN

Query Match

Best local similarity 16.7%; Score 332; DB 15; Length 350;
Matches 341; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Db 7 AGTCAAGGTTTAAATCATGATCCAGAGCCAGAGACTTTAGACATATATAGATA 66
CP 1990 AGTCAAGGTTTAAATCATGATCCAGAGCCAGAGACTTTAGACATATATAGATA 1931
Db 67 AACCAAGGCCACAGGACGACCTCCGATGCCAGATGTTCCGACAGATCCGGGACAG 126
CP 1930 AACCAAGGCCACAGGACGACCTCCGATGCCAGATGTTCCGACAGATCCGGGACAG 1871
Db 127 GGCAGTCAGAGCAGTATGTTTCCATCCTCCACTCAGAGAGAGAGAGGAGGAGAGC 186
CP 1870 GGCAGTCAGAGCAGTATGTTTCCATCCTCCACTCAGAGAGAGAGAGGAGGAGAGC 1011
Db 187 -TTCTTCACAAGGAGATGACTTTAGAGCTGCTCAGAACACCCAGTCTCCCTACCC 245
CP 1810 TTCTTCACAAGGAGATGACTTTAGAGCTGCTCAGAACACCCAGTCTCCCTACCC 1751
Db 246 TAACCTTAATCTGGAATAGCAATAGAAATGCTTAATTAATTTGGTGATCCCTGCT 305
CP 1750 TAACCTTAATCTGGAATAGCAATAGAAATGCTTAATTAATTTGGTGATCCCTGCT 1691
Db 306 AGTCAAGGAGAGGAGGCTCAGAAAGGGCTTGTTGAGAGCTGATCAG 350
CP 1690 AGTCAAGGAGAGGAGGCTCAGAAAGGGCTTGTTGAGAGCTGATCAG 1646

RESULT
LOCUS
DEFINITION
ACCESSION
NID
KEYWORDS
SOURCE
ORGANISM

7
AA049894 442 bp mRNA EST 30-DEC-1996
m11d08.r1 Soares mouse embryo NBME13.5 14.5 Mus musculus cDNA
Clone 475791 5', mRNA sequence.
AA049894
91755226
EST.
house mouse.
Mus musculus.
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Euthera; Rodentia; Sciurognathi; Muridae; Murinae;
Mus.

REFERENCE
AUTHORS

1 (bases 1 to 442)
Marras, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Gaisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Thelning, B., Wylie, T., Lennon, G., Soares, B., Wilson, R., and
Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
On Dec 31, 1996 this sequence version replaced gl:1529566.

TITLE
JOURNAL
COMMENT

Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine

FEATURES

source

Location/Qualifiers
1..442

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LNL : contact
IMAGE Consortium (info@image.llnl.gov) for further info.
MGI:286535
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 405.

BASE COUNT

79 a 142 c 122 g 99 t

ORIGIN

Query Match

Best local similarity 14.5%; Score 289; DB 22; Length 442;
Matches 363; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

Db 6 CTCGAATTGCTATGCTGTGTAATCTTTCACGACAGTGTGACCGCTGCGCAGAGCCCTAC 65
QY 689 CTCGAATTGCTATGCTGTGTAATCTTTCACGACAGTGTGACCGCTGCGCAGAGCCCTAC 748
Db 66 GGGGAGGCGATGCTCAGGAGATCCGCTCCAGCCGACCTTGGCTACCCAGCTGCGCTCC 125
QY 749 GGGGAGGCGATGCTCAGGAGATCCGCTCCAGCCGACCTTGGCTACCCAGCTGCGCTCC 808
Db 126 TTCTTGAAGAGGACAGACAGTCCAGGCTCAGAGGCTGCTGCTGCTGCTCCAGCA 185
QY 809 TTCTTGAAGAGGACAGGACAGGCTCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 868
Db 186 GAAGATGCGGGCTGTGGGAGCGCGGCTTAACACCATGCCCCAGTGGCGCTGCT 245
QY 869 AAGCAGCGGGGCTGTGGGAGCGCGGCTTAACACCATGCCCCAGTGGCGCTGCT 928
Db 246 TCTGTAAACCCCAATGCTGATGTCGCGAGCTGTGCTGCGCGGAGACCTTGTGTCA 305
QY 929 TCTGTAAACCCCAATGCTGATGTCGCGAGCTGTGCTGCGCGGAGACCTTGTGTCA 988
Db 306 TCACGCTGATGATCTCCAGACCCACTGCTCATATGATGACATCTTGGGACTTGCA 365
QY 989 TCACGCTGATGATCTCCAGACCCACTGCTCATATGATGACATCTTGGGACTTGCA 1048
Db 366 ACTGACAGTCCAGATGTGCGGCGATACCTGGGGCTGATGGAGCTCCATGACCCCA 425
QY 1049 ACAGACAGTCCAGATGTGCGGCGATACCTGGGGCTGATGGAGCTCCATGACCCCA 1108
Db 426 AACTTCATCAGCAAGGT 442
QY 1109 AACTTCATCAGCAAGGT 1125

RESULT	8	AA050083	465 bp	MRNA	EST	09-SEP-1996
LOCUS						
DEFINITION		mj08d05.r1	Soares mouse embryo	NDMEJ3.5 14.5	Mus musculus	CDNA
ACCESSION		AA050083				
NID		91529753				
KEYWORDS		EST.				
SOURCE		Mus musculus				
ORGANISM		Mus musculus				
REFERENCE						
AUTHORS		Mus.				
		1. (bases 1 to 465)				
		Marras, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,				
		Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,				
		Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,				
		Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and				
		Waterston, R.				
TITLE		The Mashu-HHMI Mouse EST Project				
JOURNAL		Unpublished (1996)				
COMMENT						
		Contact: Maria M/Mouse EST Project				
		Mashu-HHMI Mouse EST Project				
		Washington University School of Medicine				
		4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108				
		Tel: 314 286 1800				
		Fax: 314 286 1810				
		Email: mouseest@watson.wustl.edu				
		This clone is available royalty-free through LNL ; contact the				
		IMAGE Consortium (info@image.lnl.gov) for further information.				
		MG:2862241				
		Seq primer: -28M13 rev2 from Amersham				
		High quality sequence stop: 431.				
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		Location/Qualifiers				
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		/strain="C57BL/6J"				
		/note="vector: pT73-Pac (Pharmacia) with a modified				
		polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA				
		was primed with a Not I - 0190(dT) primer [5,				
		TGTTACCAATCTGAAGTGGAGCGCGCGGAATTTTATTTTATTTTATTTT				
		T 3.] , on equal amounts of mRNA from 2 13.5dp and 2				
		14.5dp embryos [total RNA provided by Minoru Ko, Wayne				
		State Univ., from 2] ; double-stranded cDNA was ligated to				
		Eco RI adaptors (Pharmacia), digested with Not I and				
		cloned into the Not I and Eco RI sites of the modified				
		pT73 vector. Library went through one round of				
		normalization, and was constructed by Bento Soares and				
		M.Felina Bonaldo."				
		/db_xref="taxon:10090"				
		/clone="475497"				
		/clone_1lb="Soares mouse embryo NDMEJ3.5 14.5"				
		/sex="unknown"				
		/rname="embryo"				
		/dev_stage="13.5-14.5dp total fetus"				
		/lab_host="DH10B"				
		<1. >465				
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ORIGIN						
		Query Match 11.7%; Score 233; DB 21; Length 465;				
		Best Local Similarity 81.5%; P:ed. No. 0.00e+00;				
		Matches 313; Conservative 0; Mismatches 69; Indels 2; Gaps 2;				
		84 CTGAATGATCGGCTCTGTGTGCTGTGCTGTGGGCGGCACCTGGAGGAGAAATCGCCTT 143				
		245 CTGATGTTGCTGCTGCTCTGCGCGCGCTGCGCTCTGCGAGCGCGAGAACCCCTT 304				
		144 GCCACGAGAACAGGTTTGTGAACAGCTGTAACCCAGGCGAGAAAGAAATGCGAGCTAAT 203				
		305 CCCACAGAAAGCGCACTATGAACAGCTGTCTCCAGGCGCAGAGAGAAATGCCAGGCTAT 364				
		204 CCCGCTTCAAGGCTGCTACCAAGCAGCCTGGGCTCTTCGACCTCCAGT-TAAGCAGGCGG 262				

	9	AA676213	189 bp	mRNA	EST	19-DEC-1997
LOCUS						
DEFINITION		z139hl12.s1 Soares fetal liver spleen INFLS S1 Homo sapiens				
ACCESSION		AA676213				
NID		92556735				
KEYWORDS		EST.				
SOURCE		human.				
ORGANISM		Homo sapiens				
		Eukaryote; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;				
		Primates; Catarrhini; Hominoidea; Hominidae; Homo.				
REFERENCE		1 (bases 1 to 189)				
AUTHORS		Hillier,L., Allen,M., Bowles,L., Dubuque,T., Giesel,G., Jost,S.,				
		Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,				
		Martin,J.J., Moore,B., Scheinberg,K., Stepec,M., Tan,F.,				
		Theising,B., White,Y., Wyllie,T., Waterston,R. and Wilson,R.				
TITLE		WashU-NCI human EST Project				
JOURNAL		Unpublished (1997)				
COMMENT		Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel.: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LLNL : contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 182. Location/Qualifiers 1..189				
FEATURES		/organism="Homo sapiens"				
source		/note="Organ: Liver and Spleen; Vector: pT7n3D (Pharmacia				
		with a modified polylinker; Site_1: Pac I; Site_2: Eco RI				
		This is a subtracted version of the original Soares fetal				
		liver spleen INFLS library. 1st strand cDNA was primed				
		with a Pac I - oligo(dT) primer [5']				
		AACGGAAGAATTAATAAGACTCTTTTTTTTTTTTTTTTTT 3'].				
		(Pharmacia), digested with Pac I and cloned into the Pac I				
		and Eco RI sites of the modified pT7n3 vector. Library				
		went through one round of normalization. Library				
		constructed by Bento Soares and M.Fatima Bonaldo."				
		/db_xref="taxon:9606"				
		/clone="433223"				
		/clone_1lb="Soares fetal liver spleen INFLS S1"				
		/sex="male"				
		/dev_stage="20 week-post conception fetus"				
		/lab_host="DH10B (ampicillin resistant)"				
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ORIGIN						
Query Match		9.1%; Score 181; DB 11; Length 189;				


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DB      61  AAAGCAAGGCCCAAGAGGCTCAGCTCCTGATGCCAGATGTTGGCAGATCCGGGGACA 120
OY      62  AAAGCAAGGCCCAAGAGGCTCAGCTCCTGATGCCAGATGTTGGCAGATCCGGGGACA 121
DB      121  GGGCAGTGCAGGAGCATGATTCTTCATCTCCACTCAGAGAGAGACGAGGG 173
OY      122  GGGCAGTGCAGGAGCATGATTCTTCATCTCCACTCAGAGAGAGAG-CGAGGGG 173

RESULT  12  AA694259  474 bp  mRNA  EST  16-DEC-1997
LOCUS    2131011.s1 Soares fetal liver spleen INFUS S1 Homo sapiens cDNA
DEFINITION clone 432405 3', mRNA sequence.
ACCESSION AA694259
NID       92695197
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
REFERENCE Eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
AUTHORS   Primates; Catarrhini; Homindae; Homo.
TITLE     1 (bases 1 to 474)
JOURNAL   Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisels, G., Jost, S.,
COMMENT   Krieman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
          Martin, J., Moore, B., Schellenberg, K., Stepien, M., Tan, F.,
          Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
          WashU-NCI human EST Project
          Unpublished (1997)

FEATURES
    source          Contact: Wilson RK
                    Washington University School of Medicine
                    4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                    Tel: 314 286 1800
                    Fax: 314 286 1810
                    Email: estewatson.wustl.edu
                    This clone is available royalty-free through LNL; contact the
                    IMAGE Consortium (info@image.lnl.gov) for further information.
                    Seq primer: -40m13 fwd. ET from Amersham
                    High quality sequence stop: 451.
                    Location/Qualifiers
                        1..474
                        /organism="Homo sapiens"
                        /note="Organ: Liver and Spleen; Vector: p773D (Pharmacia)
                        with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                        This is a subcloned version of the original Soares fetal
                        liver spleen INFUS library. 1st strand cDNA was primed
                        with a Pac I - oligo(dT) primer [5'
                        AACTGGAAGATTAATTAAGATCTTTTCTTTTCTTTT 3']
                        double-stranded cDNA was ligated to Eco RI adaptors
                        (Pharmacia), digested with Pac I and cloned into the Pac I
                        and Eco RI sites of the modified p773 vector. Library
                        went through one round of normalization. Library
                        constructed by Bento Soares and M. Fatima Bonaldo."
                        /db_xref="GDB:1332174"
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                        /clone="432405"
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                        /sex="male"
                        /dev_stage="20 week-post conception fetus"
                        /lab_host="DH10B (ampicillin resistant)"

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Best Local Similarity 97.7%; Pred. No. 2,266-238;
Matches 169; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
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OY      2  AAGTCAAAAGTTTAAATCATGATCCAAAGAGCCCAAGAGACTTTAGGACAAATTAAGGAAT 61
DB      76  AAAGCAAGGCCCAAGAGGCTCAGCTCCTGATGCCAGATGTTGGCAGATCCGGGGACA 135

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OY      62  AAAGCAAGGCCCAAGAGGCTCAGCTCCTGATGCCAGATGTTGGCAGATCCGGGGACA 121
DB      136  GGGCAGTGCAGGAGCATGATTCTTCATCTCCACTCAGAGAGAGACGAGGG 188
OY      122  GGGCAGTGCAGGAGCATGATTCTTCATCTCCACTCAGAGAGAGAG-CGAGGGG 173

RESULT  13  AA984036  350 bp  mRNA  EST  07-JUL-1998
LOCUS    oq02f02.s1 NCI_CGAP_Lus Homo sapiens cDNA clone IMAGE:1585179 3',
DEFINITION mRNA sequence.
ACCESSION AA984036
NID       93162561
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
REFERENCE Eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
AUTHORS   Primates; Catarrhini; Homindae; Homo.
TITLE     1 (bases 1 to 350)
JOURNAL   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          Tumor Gene Index
          Unpublished (1997)

FEATURES
    source          Contact: Robert Strausberg, Ph.D.
                    Tel: (301) 496-1550
                    Email: Robert_Strausberg@nih.gov
                    Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.
                    Emmert-Buck, M.D., Ph.D.
                    cDNA Library Preparation: M. Bento Soares, Ph.D.
                    cDNA Library Arrayed by: Greg Lennon, Ph.D.
                    DNA Sequencing by: Washington University Genome Sequencing Center
                    Clone distribution: NCI-CGAP clone distribution information can be
                    found through the I.M.A.G.E. Consortium/LNL at:
                    www.bio.lnl.gov/db/ftp/image/image.html
                    Insert Length: 762 Std Error: 0.00
                    Seq primer: -40m13 fwd. ET from Amersham
                    High quality sequence stop: 284.
                    Location/Qualifiers
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                        /note="Organ: Lung; Vector: p773D-Pac (Pharmacia) with
                        modified polylinker; 1st strand cDNA was prepared by
                        neuroendocrine lung carcinoid, and was then primed with
                        Not I - oligo(dT) primer. Double-stranded cDNA was
                        to Eco RI adaptors (Pharmacia), digested with Not I
                        cloned into the Not I and Eco RI sites of the
                        p773 vector. Library is normalized. Library
                        constructed by Bento Soares and M. Fatima Bonaldo."
                        /db_xref="taxon:9606"
                        /clone="IMAGE:1585179"
                        /clone_1lb="NCI_CGAP_Lus"
                        /tissue_type="carcinoid"
                        /lab_host="DH10B"

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Best Local Similarity 97.1%; Pred. No. 3,066-254;
Matches 168; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
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OY      2  AAGTCAAAAGTTTAAATCATGATCCAAAGAGCCCAAGAGACTTTAGGACAAATTAAGGAAT 61
DB      66  AAAGCAAGGCCCAAGAGGCTCAGCTCCTGATGCCAGATGTTGGCAGATCCGGGGACA 135
OY      62  AAAGCAAGGCCCAAGAGGCTCAGCTCCTGATGCCAGATGTTGGCAGATCCGGGGACA 135
DB      126  GGGCAGTGCAGGAGCATGATTCTTCATCTCCACTCAGAGAGAGAG-CGAGGGG 178

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RESULT	14		
LOCUS		W69774	450 bp mRNA EST 16-OCT-1996
DEFINITION		2448606.s1 Soares fetal heart NBHH19W Homo sapiens cDNA clone 343930 3', mRNA sequence.	
ACCESSION		W69774	
NID		91379032	
SOURCE		EST.	
ORGANISM		human.	
		Homo sapiens	
		Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
REFERENCE	1	(bases 1 to 450)	
AUTHORS		Hillier, L., Clark, N., Dubucq, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisanskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.	
TITLE		The Washu-Merck EST Project	
JOURNAL		Unpublished (1995)	
COMMENT		<p>Contact: Wilson RK</p> <p>Washu-Merck EST Project</p> <p>Washington University School of Medicine</p> <p>4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108</p> <p>Tel: 314 286 1800</p> <p>Fax: 314 286 1810</p> <p>Email: est@wustl.wustl.edu</p> <p>This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.</p> <p>Insert Length: 580 Std Error: 0.00</p> <p>Seq primer: mob.REGA-ET</p> <p>High quality sequence stop: 380.</p> <p>Location/Qualifiers</p> <p>1..450</p> <p>/organism="Homo sapiens"</p> <p>/note="Organ: heart; Vector: pT73D (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTCACATCTGACGTGGAGCGGCGCCGACATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaibo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NBHL19W."</p> <p>/db_xref="taxon:9606"</p> <p>/clone_lib="Soares fetal heart NBHH19W"</p> <p>/sex="unknown"</p> <p>/dev_stage="19 weeks"</p> <p>/lab_host="DH10B (ampicillin resistant)"</p> <p>complement(1..>450)</p>	
BASE COUNT	130 a	96 c	134 g 87 t 3 others
ORIGIN			
mRNA			
Query Match		7.9%; Score 158; DB 21; Length 450;	
Best Local Similarity	97.1%;	Pred. NO. 3.06e-254;	
Matches	168; Conservative	0; Mismatches 4; Indels 1; Gaps 1;	
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Qy	2	AAGTCAAAGGTTTAATCATCATCCAGAGCGCCGAGAGACTTTAGGACAAATATAGGAT	61
Db	62	AAACGAGCGCCACAGGCTCCAGCTCCTGATGCCGCGAGATGTCGAGAGATCCGGGAC	121
Qy	62	AAACGAGCGCCACAGGCTCCAGCTCCTGATGCCGCGAGATGTCGAGAGATCCGGGAC	121
Db	122	GGGAGTGCAGGCGAGTAGTTCCTTCATCTCCATCCAGGGGAGAG-CCAGGGG	174

[illegible]

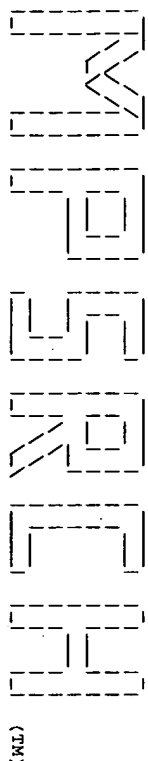
Mon Mar 15 06:28:31 1999

US-08-866-354-37.rst

Page 10

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 DB CCCGCTTTCAGAGGCTGCCTTACACAGCACCCTGGGGCTCTGCACATCTGCAGT-TAACAGAGCCG 263
 QY CCCACCTCTGAGTGTCTGCTTACCACACACCTGGATTCTCTGCACCTTACGATTAAGCACCACCA 424
 DB CTGCCCCATTAGAGGAGATCTGCCATCTCTGCACAGCTGCTTAGAGGACAGCAGAACTCAGG 323
 QY CTGCCCCATTAGAGGAGACCTTCCGGTCCCTCTGCTAGCTGCTTGGAGGACAGCAGCAACTCAGG 484
 DB AACAGCTCTCTGATAGACTGAGGAGTGCAC 352
 QY AACAGCTCTCTGATAGCTGCTGATGTGCCA 513

Search completed: Fri Mar 12 04:34:58 1999
Job time : 4622 secs.



(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution Rights by Oxford Molecular Ltd

Mparc_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Mar 8 14:13:58 1999; Maspar time 14.47 Seconds

Tabular output not generated.

Title: >US-08-866-354-38
Description: (1-400) from US08866354.pep
Perfect Score: 3033
Sequence: 1 MVRPLNRPPLPPVYVLMILL.....PWVSLSCPLILLLSLM 400

Scoring table:
PAM 150
Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

a.gensseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Statistics: Mean 34.299; Variance 146.727; scale 0.234

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	3029	99.9	400	28	Human Ret ligand RetL	7.97e-287
2	2378	78.4	315	28	Human Ret ligand RetL	1.80e-221
3	2356	77.7	397	28	Mouse Ret ligand RetL	2.89e-219
4	2074	68.4	346	28	Mouse Ret ligand RetL	5.03e-191
5	717	23.6	460	28	Human Ret ligand RetL	1.74e-56
6	701	23.1	464	28	Human Ret ligand RetL	6.25e-55
7	686	22.6	465	28	Human Ret ligand RetL	1.79e-53
8	678	22.4	468	28	Human Ret ligand RetL	1.07e-52
9	678	22.4	468	28	Human Ret ligand RetL	1.07e-52
10	678	22.4	468	28	Human Ret ligand RetL	1.07e-52
11	532	17.5	346	28	Human Ret ligand RetL	1.31e-38
12	113	3.7	1015	27	Human insulinom-asso	1.09e+00
13	113	3.7	1015	27	Human insulinom-asso	1.09e+00
14	113	3.7	1015	27	Human insulinom-asso	1.09e+00
15	110	3.6	969	24	Macaque islet cell an	8.48e+00
16	106	3.3	1021	13	Macaque islet cell an	8.48e+00
17	101	3.3	1021	13	Macaque islet cell an	8.48e+00
18	101	3.3	107	4	Human Gro beta cytol	8.48e+00

Result	1	101	107	4	R20529	Human macrophage Int1
AC	W37463:	101	107	4	R20589	Human macrophage Int1
DT	21-MAY-1998 (first entry)	3.3	107	4	R20589	Human macrophage Int1
DE	Human Ret ligand RetL3.	3.3	505	10	R55369	Human Actinin recepto
KW	Ret ligand: RetL; RetL3: receptor; signal transduction; human;	3.2	228	19	R98742	Tazarotene induced ge
KW	cell growth; renal cell; nerve cell; renal failure; nephritis;	3.2	599	4	R21690	Prostaglandin endoper
KW	kidney transplant; toxic injury; hypoxic injury;	3.2	638	25	W32098	Miniature swine retro
KW	neurodegeneration; motor neuron disease; multiple sclerosis;	3.2	1481	19	W03740	rchd528 gene product.
KW	infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;	3.1	505	10	R55373	Mouse Actinin recepto
KW	cerebral palsy; Lyme disease; muscular dystrophy;	3.1	505	13	R70240	Serine/threonine kina
KW	myasthenia gravis; tumour; therapy.	3.0	113	27	W36449	Human chemokine alpha
OS	Homo sapiens.	3.0	223	29	W43407	Human acylcoenzyme A:
PN	W09744356-82.	3.0	384	24	W23278	Bordetella pertussis
PD	27-NOV-1997.	3.0	322	19	R98744	Nuclear envelope-asso
PF	07-MAY-1997: U07726.	2.9	458	18	R22209	h-ICBP-4.
PR	10-APR-1997: US-017427.	2.9	324	4	R21833	Sequence of insulin-1
PR	08-MAY-1996: US-017427.	2.9	462	22	W09876	Arabidopsis violaxanth
PR	07-JUN-1996: US-019300.	2.9	501	18	W03760	Mullerian inhibiting
PR	16-JUL-1996: US-021859.	2.9	505	8	R41921	Canine herpesvirus q1
PA	(BIOJ) BIOGEN INC.	2.9	522	26	W23000	A. niger strain M-62
PI	Cate RL, Hesslon C, Santicola-Nadel M;	2.9	670	19	R94370	Human protocadherin-4
DR	WPI: 98-018431/02.	2.9	1026	11	R58906	Protocadherin clone 4
DR	N-PSDB: V00251.	2.9	1026	17	R87146	Inositol-1,4,5-tripho
PT	New nucleic acid encoding ret receptor ligands and related prote	2.9	1096	20	W01596	Alternatively spliced
PT	- vectors, transformed cells and antibodies, used for promoting c	2.9	1203	17	R87152	Product of alternativ
PT	growth and improving survival of injured cells, especially retin	2.9	1810	16	R94563	Chicken cytotactin
PT	nerve cells	2.8	181	3	R13369	G-CSF deriv. without
PS	Claim 2: Page 85-86: 113pp: English.					
CC	This amino acid sequence comprises human Ret ligand (RetL) RetL3,					
CC	deduced from cDNA clones (see V00251) isolated from a adult h					
CC	and spinal cord libraries. Rat and human RetL, human RetL2 and					
CC	mouse RetL sequences (see W37457-62) are also claimed. Human					
CC	RetL3 is 34.3% identical to human RetL3. 34.9% identical to human					
CC	RetL2 and 76.8% identical to murine RetL3. Ret ligand is a key					
CC	component of the Ret signalling pathway that specifically					
CC	interacts with Ret receptor protein, triggering Ret domain					
CC	and/or autophosphorylation of the Ret tyrosine kinase domain.					
CC	Vectors containing retL DNA and prokaryotic or eukaryotic host					
CC	cells transformed or transfected with these vectors are claimed,					
CC	well as a method for production of RetL3, its soluble variants,					

ALIGNMENTS

CC fusion proteins with a toxin, imageable compound or radionuclide.
 CC RetL3, optionally when expressed from vectors in vivo, is used to
 CC promote growth of new tissue and survival of damaged tissue,
 CC particularly kidney or neural tissue. Typical applications are in
 CC renal failure, nephritis, kidney transplants, toxic or hypoxic
 CC injury, neurodegeneration, motor neurone disease, multiple sclerosis,
 CC bacterial, viral or prion infections (e.g. meningitis, myelopathy
 CC associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
 CC spinal cord injury, developmental disorders such as Down's syndrome
 CC and cerebral palsy, or conditions involving the peripheral nervous
 CC system (Lyme disease, muscular dystrophy and myasthenia gravis).
 CC Fusion proteins are used to deliver toxins etc. to Ret-expressing
 CC cells, especially tumours.
 SQ Sequence 400 AA:

Query Match 99.9%; Score 3029; DB 28; Length 400;
 Best Local Similarity 99.8%; Pred. No. 7,976-287;
 Matches 399; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 mvrplrpplrpvlml11111ppsp1laagdp1pcesrlmsclqarrckgqadpcsa 60
 1 mvrplrpplrpvlml11111ppsp1laagdp1pcesrlmsclqarrckgqadpcsa 60
 Db 61 yhlldscststip1psepsvpadcleaagqlmsl1gcmchrnkqvacldiytv 120
 61 yhlldscststip1psepsvpadcleaagqlmsl1gcmchrnkqvacldiytv 120
 Db 121 hraslgyvelavspredvtakpwmksl1m1kpd6d1l1kfm1ctldkcdrlrk 180
 121 hraslgyvelavspredvtakpwmksl1m1kpd6d1l1kfm1ctldkcdrlrk 180
 Db 181 aygeacspgpcgtrhvc1rlq1ltf1fekaephaqg111cpcapndrgcgerrrntlapna 240
 181 aygeacspgpcgtrhvc1rlq1ltf1fekaephaqg111cpcapndrgcgerrrntlapna 240
 Db 181 aygeacspgpcgtrhvc1rlq1ltf1fekaephaqg111cpcapndrgcgerrrntlapna 240
 181 aygeacspgpcgtrhvc1rlq1ltf1fekaephaqg111cpcapndrgcgerrrntlapna 240
 Db 241 lrpvpapnc1elrrl1cfsd6l1crr1vd1q1tchpmd1lg1tcategrc1ray1g1lgtam 300
 241 lrpvpapnc1elrrl1cfsd6l1crr1vd1q1tchpmd1lg1tcategrc1ray1g1lgtam 300
 Db 241 lrpvpapnc1elrrl1cfsd6l1crr1vd1q1tchpmd1lg1tcategrc1ray1g1lgtam 300
 241 lrpvpapnc1elrrl1cfsd6l1crr1vd1q1tchpmd1lg1tcategrc1ray1g1lgtam 300
 Db 301 tnfnsnvtswal1sc1tgcsgn1lgeecm1egfshmpcl1ealaakmrfhsq1fsqdw 360
 301 tnfnsnvtswal1sc1tgcsgn1lgeecm1egfshmpcl1ealaakmrfhsq1fsqdw 360
 Db 301 tnfnsnvtswal1sc1tgcsgn1lgeecm1egfshmpcl1ealaakmrfhsq1fsqdw 360
 301 tnfnsnvtswal1sc1tgcsgn1lgeecm1egfshmpcl1ealaakmrfhsq1fsqdw 360
 Db 361 phrtfahmqn1pav1rpqwp1slfsc1p11111slw 400
 361 phrtfahmqn1pav1rpqwp1slfsc1p11111slw 400
 Db 361 phrtfahmqn1pav1rpqwp1slfsc1p11111slw 400
 361 phrtfahmqn1pav1rpqwp1slfsc1p11111slw 400

RESULT 2
 ID W37462 standard; Protein: 315 AA.
 AC W37462;

DT 21-MAY-1998 (first entry)
 DE Human Ret ligand RetL3 partial sequence.
 KW Cell ligand; RetL3; receptor; signal transduction; human;
 KW cell growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury;
 KW neurodegeneration; motor neurone disease; multiple sclerosis;
 KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
 KW cranial nerve injury; spinal cord injury; Down's syndrome;
 KW cerebral palsy; Lyme disease; muscular dystrophy;
 KW myasthenia gravis; tumour; therapy.
 OS Homo sapiens.
 PN M09744356-A2.
 PD 27-NOV-1997.
 PR 07-MAY-1997; 007726.
 PR 10-APR-1997; US-017427.
 PR 08-MAY-1996; US-017427.
 PR 07-JUN-1996; US-019300.
 PR 16-JUL-1996; US-021859.
 PA (BioJ) BIOGEN INC.
 PI Cate RL, Hession C, Santicola-Nadel M;
 DR WPI: 98-018431/02.
 DR N-PSDB: V00250.

PT New nucleic acid encoding ret receptor ligands and related proteins
 PT - vectors, transformed cells and antibodies, used for promoting cell
 PT growth and improving survival of injured cells, especially renal or
 PT nerve cells
 PS Claim 2; Page 81-82; 113pp: English.
 CC This amino acid sequence comprises a human Ret ligand (RetL3)
 CC partial polypeptide sequence, deduced from a partial clone (see
 CC V00250) isolated from a human adult heart cDNA library; a
 CC full-length RetL3 sequence (see W37463) is also claimed, as well
 CC as rat and human RetL1, human RetL2 and mouse RetL3 sequences
 CC (see W37455-61). Ret ligand is a key component of the Ret
 CC signalling pathway that specifically interacts with Ret receptor
 CC protein, triggering Ret dimerisation and/or autophosphorylation of
 CC the Ret tyrosine kinase domain. Vectors containing RetL3 DNA and
 CC prokaryotic or eukaryotic host cells transformed or transfected
 CC with these vectors are claimed, as well as a method for production
 CC of RetL3, its soluble variants and fusion proteins with a toxin,
 CC imageable compound or radionuclide. RetL3, optionally when
 CC expressed from vectors in vivo, is used to promote growth of new
 CC tissue and survival of damaged tissue, particularly kidney or
 CC neural tissue. Typical applications are in renal failure,
 CC nephritis, kidney transplants, toxic or hypoxic injury,
 CC neurodegeneration, motor neurone disease, multiple sclerosis,
 CC bacterial, viral or prion infections (e.g. meningitis, myelopathy
 CC associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
 CC spinal cord injury, developmental disorders such as Down's syndrome
 CC and cerebral palsy, or conditions involving the peripheral nervous
 CC system (Lyme disease, muscular dystrophy and myasthenia gravis).
 CC Fusion proteins are used to deliver toxins etc. to Ret-expressing
 CC cells, especially tumours.
 SQ Sequence 315 AA:

Query Match 78.4%; Score 2378; DB 28; Length 315;
 Best Local Similarity 99.0%; Pred. No. 1,806-221;
 Matches 308; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 5 tpg1nns1lgcmchrnkqvacldiytvhrars1gnyel1dspyedvtspkwm1 64
 5 tpg1nns1lgcmchrnkqvacldiytvhrars1gnyel1dspyedvtspkwm1 64
 Db 90 aqolrns1lgcmchrnkqvacldiytvhrars1gnyel1dspyedvtspkwm1 149
 90 aqolrns1lgcmchrnkqvacldiytvhrars1gnyel1dspyedvtspkwm1 149
 Db 65 sk1m1kpd6d1l1kfm1ctldkcdrl1rayeacspgpcgtrhvc1rlq1ltf1feka 124
 65 sk1m1kpd6d1l1kfm1ctldkcdrl1rayeacspgpcgtrhvc1rlq1ltf1feka 124
 Db 150 sk1m1kpd6d1l1kfm1ctldkcdrl1rayeacspgpcgtrhvc1rlq1ltf1feka 209
 150 sk1m1kpd6d1l1kfm1ctldkcdrl1rayeacspgpcgtrhvc1rlq1ltf1feka 209
 Db 125 phaag111cpcapndrgcgerrrntlapna1pav1rpqwp1slfsc1p11111slw 184
 125 phaag111cpcapndrgcgerrrntlapna1pav1rpqwp1slfsc1p11111slw 184
 Db 210 phaag111cpcapndrgcgerrrntlapna1pav1rpqwp1slfsc1p11111slw 269
 210 phaag111cpcapndrgcgerrrntlapna1pav1rpqwp1slfsc1p11111slw 269
 Db 185 tchpmd1lg1tcategrc1ray1g1lgtam1pfn1vntswal1sc1tgcsgn1lgeec 244
 185 tchpmd1lg1tcategrc1ray1g1lgtam1pfn1vntswal1sc1tgcsgn1lgeec 244
 Db 270 tchpmd1lg1tcategrc1ray1g1lgtam1pfn1vntswal1sc1tgcsgn1lgeec 320
 270 tchpmd1lg1tcategrc1ray1g1lgtam1pfn1vntswal1sc1tgcsgn1lgeec 320
 Db 245 m1egfshmpcl1ealaakmrfhsq1fsqdw1phtfahmqn1pav1rpqwp1slfsc 303
 245 m1egfshmpcl1ealaakmrfhsq1fsqdw1phtfahmqn1pav1rpqwp1slfsc 303
 Db 330 m1egfshmpcl1ealaakmrfhsq1fsqdw1phtfahmqn1pav1rpqwp1slfsc 360
 330 m1egfshmpcl1ealaakmrfhsq1fsqdw1phtfahmqn1pav1rpqwp1slfsc 360
 Db 305 t1p11111slw 315
 305 t1p11111slw 315
 Db 390 t1p11111slw 400
 390 t1p11111slw 400

RESULT 3
 ID W37461 standard; Protein: 397 AA.
 AC W37461;

DT 21-MAY-1998 (first entry)
 DE Mouse Ret ligand RetL3.
 KW Mouse Ret ligand; RetL3; receptor; signal transduction; mouse;
 KW cell growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury;
 KW neurodegeneration; motor neurone disease; multiple sclerosis;
 KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
 KW cranial nerve injury; spinal cord injury; Down's syndrome;
 KW cerebral palsy; Lyme disease; muscular dystrophy;

AC W37459; (first entry)
 DT 21-MAY-1998
 DE Human Ret ligand RetL.
 KW Ret ligand; RetL; receptor; signal transduction; human;
 KW cell growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury;
 KW neurodegeneration; motor neurone disease; multiple sclerosis;
 KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
 KW cranial nerve injury; spinal cord injury; Down's syndrome;
 KW cerebral palsy; Lyme disease; muscular dystrophy;
 KW myasthenia gravis; tumour; therapy.
 OS Homo sapiens.
 PN MO9744356-A2.
 PD 27-NOV-1997.
 PE 07-MAY-1997; U07726.
 PR 10-APR-1997; US-017427.
 PR 08-MAY-1996; US-017427.
 PR 07-JUN-1996; US-019300.
 PR 16-JUL-1996; US-021859.
 PA (BioJ) BIOGEN INC.
 PI Cate RL, Hession C, Santicola-Nadel M;
 DR MPI: 98-018431/02.
 DR N-PSDB: V00247.
 PT New nucleic acid encoding ret receptor ligands and related proteins
 PT - vectors, transformed cells and antibodies, used for promoting cell
 PT growth and improving survival of injured cells, especially renal or
 PT nerve cells
 PS Claim 2: Page 64-66; 113pp; English.
 CC This amino acid sequence comprises human Ret ligand (RetL) RetL,
 CC deduced from cDNA clones (see V00247) isolated from a human
 CC foetal kidney. Rat RetL and mouse and human RetL2 and RetL3
 CC sequences (see W37457 and W37460-63) are also claimed. The
 CC human RetL sequence is 93.3% identical to that of rat. Ret ligand
 CC is a key component of the Ret signalling pathway that specifically
 CC interacts with Ret receptor, triggering Ret dimerisation and/or
 CC autophosphorylation of the Ret tyrosine kinase domain. Vectors
 CC containing retL DNA and prokaryotic or eukaryotic host cells
 CC transformed or transfected with these vectors are claimed, as well
 CC as a method for production of RetL, its soluble variants and fusion
 CC proteins with a toxin, imageable compound or radionuclide. RetL,
 CC optionally when expressed from vectors in vivo, is used to promote
 CC growth of new tissue and survival of damaged tissue, particularly
 CC kidney or neural tissue. Typical applications are in renal failure,
 CC nephritis, kidney transplants, toxic or hypoxic injury,
 CC neurodegeneration, motor neurone disease, multiple sclerosis,
 CC bacterial, viral or prion infections (e.g. meningitis, myelopathy
 CC associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
 CC spinal cord injury, developmental disorders such as Down's syndrome
 CC and cerebral palsy, or conditions involving the peripheral nervous
 CC system (Lyme disease, muscular dystrophy and myasthenia gravis).
 CC Fusion proteins are used to deliver toxins etc. to Ret-expressing
 CC cells, especially tumours.
 SQ Sequence 460 AA;
 Query Match 23.6%; Score 717; DB 28; Length 460;
 Best Local Similarity 36.5%; Pred. No. 1,74e-56;
 Matches 125; Conservative 69; Mismatches 129; Indels 19; Gaps 17;
 Db 6 lyfalpldlilisa-e-vsggdl-d-cvkaadqclkegscetyrltgcvgakctnfs 61
 Qy 17 LLLLLPSPPLAAGPLPTESRLMNSCLQARRCCQADPTCSAAYHLLDCTSSISPTLP 76
 Db 62 laasgleekdecraamealjkxslyncrcrgmkkekncrltlywamygsdq-gndldesp 120
 Qy 77 -SEEPSVPADCLEAQAOLRRSSSLIGCMCHRRKNQVACLDIYTWVHARSGLVETDVP 135
 Db 121 ye-pvnarlsladifrvpflisvehlipkynclidaakacnldldckkyrsayltcctsvsn 179
 Qy 136 YEDTVTSKPKM-NLSK-LMLK-PPSDCLCFKAMCTLNDKDRLRKAAGCAES-G-PH 190
 Db 180 dvcnrkckhalklqgfdkcpaksgymlfsc--rdlaacterrrtqtltpvcysyeekpn 237
 Qy 191 --CORHVCRLQLTLTFEKAEPHQAOGILLCPCAPBNDRCGERRRNTIAPCALPVA-PN 247

Db 238 cnlqgscctnylccrcladffncqpearsvscikenyadcllqslgtvmtpnyl 297
 Qy 248 CLELRCLCRSDPLCRRLVDFQTHCPMDI-LGTATEQ-SNCLRAYLGLISTAMPNRA 305
 Db 298 dssajsvapwcdsngndleoclklfnlfnkntclkaqla 339
 Qy 306 SNNVTSVALSCRCRSGNLOEBCMELEGFSSNPLCTEIAIA 347
 RESULT 6
 ID W37460 standard; Protein: 464 AA.
 AC W37460;
 DT 21-MAY-1998 (first entry)
 DE Human Ret ligand RetL2.
 KW Ret ligand; RetL2; receptor; signal transduction; human;
 KW cell growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury;
 KW neurodegeneration; motor neurone disease; multiple sclerosis;
 KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
 KW cranial nerve injury; spinal cord injury; Down's syndrome;
 KW cerebral palsy; Lyme disease; muscular dystrophy;
 KW myasthenia gravis; tumour; therapy.
 OS Homo sapiens.
 PN MO9744356-A2.
 PD 27-NOV-1997.
 PE 07-MAY-1997; U07726.
 PR 10-APR-1997; US-017427.
 PR 08-MAY-1996; US-017427.
 PR 07-JUN-1996; US-019300.
 PR 16-JUL-1996; US-021859.
 PA (BioJ) BIOGEN INC.
 PI Cate RL, Hession C, Santicola-Nadel M;
 DR MPI: 98-018431/02.
 DR N-PSDB: V00248.
 PT New nucleic acid encoding ret receptor ligands and related proteins
 PT - vectors, transformed cells and antibodies, used for promoting cell
 PT growth and improving survival of injured cells, especially renal or
 PT nerve cells
 PS Claim 2: Page 69-70; 113pp; English.
 CC This amino acid sequence comprises human Ret ligand (RetL) RetL,
 CC deduced from a cDNA clone (see V00248) isolated from a human foetal
 CC liver library. Rat and human RetL1, and human and mouse RetL2
 CC sequences (see W37457-59 and W37461-63) are also claimed. Human
 CC RetL2 is 49.1% identical to human RetL1 protein. RetL is a
 CC key component of the Ret signalling pathway that specifically
 CC interacts with Ret receptor protein, triggering Ret dimerisation
 CC and/or autophosphorylation of the Ret tyrosine kinase domain.
 CC Vectors containing retL2 DNA and prokaryotic or eukaryotic host
 CC cells transformed or transfected with these vectors are claimed, as
 CC well as a method for production of RetL2, its soluble variants and
 CC fusion proteins with a toxin, imageable compound or radionuclide.
 CC RetL2, optionally when expressed from vectors in vivo, is used to
 CC promote growth of new tissue and survival of damaged tissue,
 CC particularly kidney or neural tissue. Typical applications are in
 CC renal failure, nephritis, kidney transplants, toxic or hypoxic
 CC injury, neurodegeneration, motor neurone disease, multiple sclerosis,
 CC bacterial, viral or prion infections (e.g. meningitis, myelopathy
 CC associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
 CC spinal cord injury, developmental disorders such as Down's syndrome
 CC and cerebral palsy, or conditions involving the peripheral nervous
 CC system (Lyme disease, muscular dystrophy and myasthenia gravis).
 CC Fusion proteins are used to deliver toxins etc. to Ret-expressing
 CC cells, especially tumours.
 SQ Sequence 464 AA;
 Query Match 23.1%; Score 701; DB 28; Length 464;
 Best Local Similarity 35.7%; Pred. No. 6.25e-55;
 Matches 115; Conservative 87; Mismatches 95; Indels 25; Gaps 18;
 Db 40 cvrnlcaaesncsrytlrqlag-rdr-ntlan--kcgaaalevgsplydcrc 95
 Qy 44 CLOARRCCQADPTCSAAYHLLDCTSSISPTLPSEPSVPADCLEAQAOLRRSSSLIGCMC 103

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MPSrch_PP protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Mar 8 14:16:14 1999; Maspar time 21.09 Seconds

Tabular output not generated. 710.686 Million cell updates/sec

Title: >US-08-866-354-38
Description: (1-400) from US08866354..pep
Perfect Score: 3033
Sequence: 1 MVRPLNRPPLPVVLMLL.....PMVPSLFSCTPLILLSLM 400

Scoring table:
PAM 150
Gap 11

Searched: 116738 segs, 37463448 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: p1r58
1:p1r1.2:p1r2.3:p1r3.4:p1r4

Statistics: Mean 45.680; Variance 83.673; scale 0.546

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	2356	77.7	397	2	JE0082	GPI-linked receptor -	0.00e+00
2	126	4.2	117	2	S52612	probable membrane pro	4.51e-05
3	116	3.8	354	1	XVFCO2	adaptive response reg	1.53e-03
4	113	3.7	345	2	AS3138	gastrin homolog - human	4.26e-03
5	113	3.7	1015	2	JC5263	transmembrane tyrosin	4.26e-03
6	113	3.7	1015	2	JC5062	peptidyl - human	4.26e-03
7	113	3.7	1313	2	JC3038	peptidyl-dipeptidase	1.17e-02
8	110	3.6	384	2	S25771	gastrin protein - mouse	1.17e-02
9	108	3.6	1309	2	S35484	peptidyl-dipeptidase	2.27e-02
10	106	3.5	496	2	A69601	ATP-dependent DNA hel	4.38e-02
11	103	3.4	520	1	XVFCO2	adaptive response reg	1.16e-01
12	104	3.4	352	2	S36489	L2 protein - human pa	8.38e-02
13	101	3.3	107	2	JH0281	macrophage inflamma	2.18e-01
14	101	3.3	476	2	I80182	activin type I recept	2.18e-01
15	101	3.3	487	2	I80183	activin type I recept	2.18e-01
16	100	3.3	2918	2	AS4105	fibrinogen-2 precursor	2.99e-01
17	97	3.2	61	1	DNPBF	DNA-binding protein -	7.58e-01
18	97	3.2	151	2	S33621	ADRI-2 protein - soy	7.58e-01
19	96	3.2	599	2	A36746	prostaglandin-endope	1.03e+00
20	97	3.2	607	2	I37560	protein-tyrosine kina	7.58e-01
21	98	3.2	2448	2	S35999	pyoverdine synthetase	5.57e-01
22	94	3.1	101	2	B28414	growth-regulated prot	1.88e+00
23	93	3.1	133	2	JC2202	secretin - mouse	2.54e+00

24	95	3.1	175	2	I46199	erythropoietin - dog	1.39e+00
25	95	3.1	188	1	I46083	erythropoietin precu	1.39e+00
26	93	3.1	239	2	S68257	phospholipase C (EC 3	2.54e+00
27	95	3.1	271	2	G64783	ylid protein - Escher	1.39e+00
28	94	3.1	602	2	S69198	prostaglandin G/H syn	1.88e+00
29	93	3.1	631	1	A48346	cell fusion glycoprot	2.54e+00
30	93	3.1	631	1	VGNZPD	cell fusion glycoprot	2.54e+00
31	93	3.1	1049	2	A37079	fibronectin receptor	2.54e+00
32	95	3.1	1053	2	S44250	integrin alpha-5 chain	1.39e+00
33	95	3.1	1102	2	UH0717	guanylate cyclase (EC	1.39e+00
34	94	3.1	1217	2	A45493	phospholipase C-beta	1.88e+00
35	90	3.0	241	2	A64454	hypothetical protein	6.11e+00
36	91	3.0	250	2	S71348	Rieske iron sulfur pr	4.57e+00
37	90	3.0	251	2	S20455	pgc protein - Klebsi	6.11e+00
38	92	3.0	252	2	D32252	gene I protein - Actin	3.41e+00
39	90	3.0	425	2	E71075	probable protein gluta	6.11e+00
40	91	3.0	464	2	A65558	retinoic acid recepto	4.57e+00
41	91	3.0	505	2	I38859	activin A receptor, t	4.57e+00
42	92	3.0	602	2	S39782	cyclooxygenase 1 - ra	3.41e+00
43	92	3.0	651	2	S73558	phosphate transport s	4.57e+00
44	90	3.0	699	2	S27768	RNA-directed DNA poly	6.11e+00
45	90	3.0	1868	2	S48938	hypothetical protein	6.11e+00

ALIGNMENTS

RESULT	ENTRY	1
TITLE	JE0082	#type complete
ALTERNATE_NAMES	GPI-linked receptor - mouse	
ORGANISM	GFRAlpna-3	
DATE	21-May-1998	#sequence_revision 29-May-1998 #text_change

ACCESSIONS
JE0082
REFERENCE
JE0082
#authors
#journal
#title

#accession JE0082
#molecule_type mRNA
#residues 1-397 #label NOM

COMMENT
#cross-references DBJ:AB008833; NID:92627159; PID:92627159
This protein plays a distinct role in cell survival and differentiation.

KEYWORDS
FEATURE
1-25
380-397
92,145,306
glycoprotein

SUMMARY
Query Match
Best Local Similarity 77.7%; Score 2356; DB 2; Length 397;
Matches 306; Conservative 53; Mismatches 31; Indels 3; Gaps
#domain signal sequence #status predicted #label
#region hydrophobic
#binding site carbohydrate (asn) (covalent) #status
predicted

Db	7	PRPPLMTLLVLSIW-IPLAGNSLATENRFVNSCTOARRKCEAPACKAAYOHIGST	47
Qy	9	PLPVPVMTLLILPPSPPLAAGDPLPESRLMNSCLQARRKCAADPTCSAAVHHHNS	11
Db	66	SLSRPLPLEESASADCLFAEOLRNSLIDCCHRMKQACLDIYVHVHNS	11
Qy	69	SSISTPLSEPSVPADCLFAAQQLRNSSLIGCHRRMKQVACLDIYVHVHNS	11
Db	126	YELDVSPYEDVTSTKPMKMNLSKLNMLKPDSDLCFKFAMLTCLDKDCRLKAGCA	78
Qy	129	YELDVSPYEDVTSTKPMKMNLSKLNMLKPDSDLCFKFAMLTCLDKDCRLKAGCA	78
Db	186	TRCORHCLLAOLRSFEFEKAESHAQGLLPCAPADAGCGERRNTTAPSCALPVS	245
Qy	189	PHCORHCLRLTLTFEFAAEPHAQGLLPCAPADAGCGERRNTTAPSCALPVS	248

[illegible]

```

#journal      J. Biol. Chem. (1985) 260:7281-7288
#title        Purification and structure of the intact Ada regulatory
               protein of Escherichia coli K12, O(6)-methylguanine-DNA
               methyltransferase.
#cross-references MUID:85207761
#accession    A22630
##molecule_type DNA
##residues    1-133,'R','135-354' ##label NAK
##cross-references GB:M10211; NID:g145186; PID:g145189
##experimental_source strain K12
REFERENCE
#authors      Dempsey, B.; Sedgwick, B.; Robins, P.; Toty, N.; Waterfield,
               M.D.; Lindahl, T.
#journal      Proc. Natl. Acad. Sci. U.S.A. (1985) 82:2688-2692
#title        Active site and complete sequence of the suicidal
               methyltransferase that counters alkylation mutagenesis.
#cross-references MUID:85190562
#accession    A22667
##molecule_type DNA
##residues    1-74,'D','76-78','PR','81-317','V','319-329','S','331-354'
               ##label DDM
##cross-references GB:M10315; NID:g145190; PID:g145191
##experimental_source strain B/Y
REFERENCE
#authors      Nakabeppu, Y.; Sekiguchi, M.
#journal      Proc. Natl. Acad. Sci. U.S.A. (1986) 83:6287-6301
#title        Regulatory mechanisms for induction of synthesis of repair
               enzymes in response to alkylating agents: Ada protein acts
               as a transcriptional regulator.
#cross-references MUID:86313568
#accession    I41114
##status      translated from GB/EMBL/DDBJ
##molecule_type DNA
##residues    1-27 ##label RBS
##cross-references GB:M13828; NID:g145196; PID:g145197
REFERENCE
#authors      Teo, I.; Sedgwick, B.; Kilpatrick, M.W.; McCarthy, T.V.;
               Lindahl, T.
#journal      Cell (1986) 45:315-324
#title        The intracellular signal for induction of resistance to
               alkylating agents in e. coli.
#cross-references MUID:86189944
#accession    I41115
##status      translated from GB/EMBL/DDBJ
##molecule_type DNA
##residues    1-29 ##label RB2
##cross-references GB:M13155; NID:g145198; PID:g145199
COMMENT       This enzyme has an inducible DNA repair system that protects
               against methylating and alkylating agents by transferring the
               alkyl group from O(6)-alkylguanine in DNA to a cysteine residue
               located within the enzyme itself.
GENETICS
#gene         ada
#map_position 48 min
CLASSIFICATION
#superfamily  adaptive response regulatory protein:
               methylated-DNA--protein-cysteine S-methyltransferase:
               homology: methylphosphotriester-DNA methyltransferase:
               homology
KEYWORDS       DNA binding; DNA repair; methyltransferase; transcription;
               regulation; transferase
FEATURE
7-191          domain methylphosphotriester-DNA methyltransferase:
               homology #label MPY\
268-348        domain methylated-DNA--protein-cysteine
               S-methyltransferase homology #label MGT
SUMMARY
#length 354   #molecular-weight 39323 #checksum 7668
               3.8%; Score 116; DB 1; Length 354:
Query Match Best Local Similarity 31.1%; Pred. No. 1,53e-03;
Matches 23; Conservative 17; Mismatches 29; Indels 5; Gaps
:: RTTGIFCR-PSCARRHA-LRENVSYANASDALAGFRPCKCOPEKXANAOQHRLAKTH

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Db 123 YEASPEYITSRSLDIFRLASIFSGMDPATNSKNHCLDAKACNLNDCKRLSGYST 182
QY 132 DVSPYEDIVT--SKPMKN-NL-SKLN-MLKPSDCLCFALMCLTNDKCDLRAKAYGA 185
Db 183 CSKEISATEHCGRKCHALROFEDNVSEYTYRLFCSC--KDOACAPRRQTIIVPCS 240
QY 186 CS---GP--HCORHVCRLQLLTFEERKAEPHAQGLLCPACPNDRGCGERRRNTIAPNCA 240
Db 241 YEDKRPNCJDLRNYCRADHLCRSLADPHANCOASFOSTLSCPGDNTQACLGSTGLIG 300
QY 241 LPPVA-PNCELEIRUCFSDPLCRSLVDFQTHCHP-MDLGTCACQESR-CRATLGLIG 297
Db 301 EMDTNYVDASTITITISPCSCSGNLECEKFLRDETPENCLRNAIOA 352
QY 298 TMTNTPNSVNTSVALS--CTCRSGNLECEKFLRDETPENCLRNAIOA 347

RESULT 2
AC GDNF_CHICK STANDARD: PRT: 469 AA.
ID 013156:
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF-BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 1).
DE GFRAL OR GDNFRA.
OS GALLUS GALLUS (CHICKEN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
OC GALLIFORMES.
RN [1]
RP SEQUENCE FROM N.A.
RC BUJ-BELLO A., ADU J., PINON L.G.P., HORTON A., THOMPSON J., ROSENTHAL A., CHINCHETRU M., BUCHMAN V.L., DAVIES A.M.;
RA NATURE 387:721-724(1997).
RL
CC -1- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR (BY SIMILARITY).
CC -1- SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE THOUGHT TO FORM A COMPLEX WITH THE DISULFIDE-LINKED GDNF DIMER AND WITH 2 MOLECULES OF RET (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.
CC DR EMBL: U90541; G2213803; -
KW RECEPTOR; GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL.
FT SIGNAL 1 27
FT CHAIN 28 430
FT PROPEP 431 469
FT DOMAIN 361 368
FT CARBOHYD 62 62
FT CARBOHYD 163 163
FT CARBOHYD 346 346
FT CARBOHYD 405 405
FT LIPID 430 430
FT SEQUENCE 469 AA; 52043 MW; C8D241C9 CRC32;

Query Match 24.6%; Score 746; DB 1; Length 469;
Best Local Similarity 36.7%; Pred. No. 3,726-154;
Matches 127; Conservative 69; Mismatches 132; Indels 18; Gaps 15;

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QY 132 DVSPYE--DVTSKPMKN-LSKLMLKPSDCLCFALMCLTNDKCDLRAKAYGAC-S 187
Db 180 STSNEICKRCHALALFFPKVPKSYGLFESC--RDVACERRQTIIVPCSEDR 237
QY 188 G-PH--CORHVCRLQLLTFEERKAEPHAQGLLCPACPNDRGCGERRRNTIAPNCA 240
Db 238 EKPCLNIOESCKRNYICRSLADFTNCOPESSVSCLEKENYADCLLAVSGLIGT 240
QY 245 A-PNCELEIRUCFSDPLCRSLVDFQTHCHMDI-LGTCAEQ-SRLRAYLGITAT 347
Db 298 PNYDSSLSVAPWCDCNSGNDIDECRFLNEFDQNTCKMAIOA 343
QY 302 PNFASVNTSVALSCTCRSGNLECEKFLRDETPENCLRNAIOA 347

RESULT 3
AC GDNF_MOUSE STANDARD: PRT: 463 AA.
ID 008842:
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE NEURTURIN RECEPTOR ALPHA PRECURSOR (NTRN-ALPHA) (NTRN-ALPHA) (TGF-BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 2) (GDNF RECEPTOR BETA) (GDNFR-BETA).
DE GFR2 OR GDNFRB OR TRNR2.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97325791.
RA BALOH R.H., TANSEY M.G., GOLDEN J.P., CREEDON D.J., HEUCKEROH R.O., KECK C.L., ZIMONJIC D.B., POPESCU N.C., JOHNSON E.M. JR., MIERANDT J.;
RL NEURON 18:793-802(1997).
CC -1- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NTRN-INDUCED AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET KINASE. ALSO ABLE TO MEDIATE GDNF SIGNALING THROUGH THE RET TYROSINE KINASE RECEPTOR.
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: NEURONS OF THE SUPERIOR CERVICAL AND DORSAL ROOT GANGLIA, AND ADULT BRAIN AND TESTIS. LOW LEVEL IN THE SPLEEN AND IN THE ADRENAL.
CC -1- ALTERNATIVE PRODUCTS: A SHORT FORM IS PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.
CC DR EMBL: AF002701; G2145082; -
KW RECEPTOR; GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL;
FT SIGNAL 1 21
FT CHAIN 22 443
FT PROPEP 444 463
FT CARBOHYD 52 52
FT CARBOHYD 357 357
FT CARBOHYD 413 413
FT LIPID 443 443
FT VARSUCLC 14 146
FT SEQUENCE 463 AA; 51598 MW; 0A2165C0 CRC32;

Query Match 23.3%; Score 707; DB 1; Length 463;
Best Local Similarity 36.2%; Pred. No. 3,976-144;
Matches 117; Conservative 83; Mismatches 96; Indels 27; Gaps 15;

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 W P I S R E L I F
 (TM)

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Mparch_n n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Fri Mar 12 10:00:56 1999; Maspar time 355.59 Seconds
 847.489 Million cell updates/sec

Tabular output not generated.

Title: >US-08-866-354-39
 Description: (1-2215) from US08866354.seq
 Perfect Score: 2215
 N.A. Sequence: 1 GCGGCGCGCTGACCTTGAC.....ACAGACTCGACGCGCGCGC 2215
 Comp: GCGGCGCGCTGACCTGACCTG.....TGTGTGACGCTGCGCGCGCGC

Scoring table: TABLE default
 Gap 6

Nmatch STD: Dbase 0; Query 0

Searched: 188442 seqs, 68026449 bases x 2

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database:

n-geneseq32
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19 20:part20 21:part21 22:part22 23:part23
 24:part24 25:part25 26:part26 27:part27 28:part28
 29:part29 30:part30 31:part31 32:part32 33:part33
 34:part34 35:part35 36:part36 37:part37 38:part38
 39:part39 40:part40

Statistics: Mean 9.676; Variance 5.422; scale 1.785

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	1159	52.3	1888	39	Human Ret ligand retL	0.00e+00
2	285	12.9	453	37	Human EST-derived seq	1.23e-185
3	246	11.1	351	37	Human EST-derived seq	1.90e-156
4	213	9.6	2138	38	Rat glial cell line-d	6.89e-132
5	213	9.6	3616	39	Rat Ret ligand retL1	6.89e-132
6	210	9.5	2378	37	Rat glial cell derive	2.10e-130
7	210	9.5	2568	38	Human glial cell line	1.16e-129
8	175	7.9	201	37	Human EST-derived seq	8.03e-104
9	175	7.9	201	37	Human EST-derived seq	8.03e-104
10	166	7.5	1223	39	Human Ret ligand retL	3.22e-97
11	166	7.5	1682	39	Human Ret ligand retL	3.22e-97
12	125	5.6	840	37	Mouse GDNF alpha c10	1.94e-67
13	49	2.2	14704	3	PKS 741 Insert contg.	4.25e-15

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
14	49	2.2	14704	3	PKS 741 Insert contg.	4.25e-15
15	46	2.1	91	29	Repeat sequence from	3.26e-13
16	46	2.1	200	29	Polymorphic repeat se	3.26e-13
17	46	2.1	219	4	Fragile X diagnostic	7.72e-14
18	47	2.1	282	4	Fragile X diagnostic	7.72e-14
19	47	2.1	3381	33	Porphylin-accumulatin	7.72e-14
20	47	2.1	3381	33	Porphylin-accumulatin	7.72e-14
21	46	2.1	10266	22	Mouse SRX-related gen	3.26e-13
22	44	2.0	70	5	Microsatellite sequen	3.26e-13
23	44	2.0	86	5	Microsatellite sequen	3.26e-13
24	44	2.0	91	9	Oligonucleotide prim	3.26e-13
25	45	2.0	266	4	Fragile X diagnostic	7.72e-14
26	45	2.0	382	10	Graveyine ribosomal c	1.94e-67
27	45	2.0	448	35	Graveyine ribosomal c	1.94e-67
28	45	2.0	2775	25	Pennaeus vannamei geno	1.94e-67
29	44	2.0	3404	4	Rat androgen receptor	3.26e-13
30	44	2.0	3791	29	Rat dopamine transpor	5.07e-12
31	45	2.0	4157	40	Chicken beta-actin pr	5.07e-12
32	45	2.0	4157	40	5-aminolevulinic acid	1.37e-11
33	44	2.0	4253	34	Aspergillus oryzae 5-	5.67e-12
34	45	2.0	13011	35	Human MLN 51 nucleoti	1.37e-11
35	43	1.9	61	29	CDNA encoding rat cyt	2.34e-11
36	43	1.9	64	5	Repeat sequence from	2.34e-11
37	43	1.9	65	29	Microsatellite sequen	2.34e-11
38	43	1.9	89	29	Repeat sequence from	2.34e-11
39	43	1.9	230	29	Repeat sequence from	2.34e-11
40	43	1.9	1570	17	Polymorphic repeat se	2.34e-11
41	43	1.9	1606	17	Mouse B7-1 exons 1, 2	2.34e-11
42	43	1.9	1888	17	Mouse B7-1 exons 1, 2	2.34e-11
43	43	1.9	2446	17	Rat biglycan cDNA.	2.34e-11
44	43	1.9	2516	17	Mouse B7-1 exons 1, 2	2.34e-11
45	43	1.9	2997	17	Mouse B7-1 exons 1, 2	2.34e-11

ALIGNMENTS

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	1159	52.3	1888	39	Human Ret ligand retL	0.00e+00
2	285	12.9	453	37	Human EST-derived seq	1.23e-185
3	246	11.1	351	37	Human EST-derived seq	1.90e-156
4	213	9.6	2138	38	Rat glial cell line-d	6.89e-132
5	213	9.6	3616	39	Rat Ret ligand retL1	6.89e-132
6	210	9.5	2378	37	Rat glial cell derive	2.10e-130
7	210	9.5	2568	38	Human glial cell line	1.16e-129
8	175	7.9	201	37	Human EST-derived seq	8.03e-104
9	175	7.9	201	37	Human EST-derived seq	8.03e-104
10	166	7.5	1223	39	Human Ret ligand retL	3.22e-97
11	166	7.5	1682	39	Human Ret ligand retL	3.22e-97
12	125	5.6	840	37	Mouse GDNF alpha c10	1.94e-67
13	49	2.2	14704	3	PKS 741 Insert contg.	4.25e-15

D	317	gcccacagatagatgagccgttagccgcacagggagcccttgaagcagaagagctcttgaacacac	376
Q	890	gcccacatTAAGAGATGTCACAGGACGACCCCTCGAGATCTTTCACAGAAACCCCACTGATAGACTG	949
D	377	ccgcctgcacagccgggcatatgaagaagaagaatctgtctcgatctactctatctgacatgta	436
Q	950	cccgctgcAAGCGGGGCGATGAAAGAGAGAGCTGCAGTGTCTCAATATCTACTAGGAGCATCA	100
D	437	ccgaagacgtt -cag -ggaaatggccccccgggaagatctccgcgtatgagcaggttaacag	493
Q	1010	TCCTGGGCTGCACAGGGGTGAGGATTCATGAAGCTTCCCTCATGAGCTCTGTGACTTC	106
D	494	caggcttgcagatatattccgggcagctcccgatcatalcatcagatgatttccacagaatgga	553
Q	1070	GGCGCTCTCGGACATCTTCAGGGCTCGCTTCAATCTTCTCAGGGGACAGGACAGACCCGGG	112
D	554	acacatttccaaagagaaacaactgtcctgtgacgcagccaaagcctgtcaactgtgagacac	613
Q	1130	GGTAGTAGCAAAAGACCAACCACTGCTGGATGGCGCCACAGGCTGTGCACCTTGATATACAA	118
D	614	ctgcaagaagatagagtgctgcgacctacatcacccccctgtga -ccacacaga -ctgcaac -ga	670
Q	1190	CTCGAAGAGAGTTGGCTCTCTTATATCTCATCTGCAACCGTAGATCTCTCCACCGA	124
D	671	ggctctcaaccgccgttaagtgtgcacaaagccctcagagcagttcttcgacaaggttccgag	730
Q	1250	ACGCTGCACACCGCGCAAGTGCCACCAAGGCTGTGCGCCAGTCTTTGACCGTGTGCCACAG	130
D	731	caaacacagagccagagatgtctctctgtctctctccggagatatcgctctcaaccgaagcgag	790
Q	1310	CGAGTATACCTACCGCATGCTCTTCTCTCTCTGTGACAGACAGCATGTGCTGAGGTGG	136
D	791	gcgcacagactatcgtctcccgctgtgtctctta tgaagaacgagagagggcccaactgcctgag	850
Q	1370	CCGGCAACACATCTCTGCCAGTGGTCTCTTGAAGGACAAAGAAAGGCCAATGCTCGGA	142
D	851	ctgtcgaagatctccgtgcgaagcccaattatctatctgcagatctcgcctctgcagattttttac	910
Q	1430	CTGTGCGAGCGTTGTGTGTACAGCCCACTGTGCTCCGGTCCGAGTGGCAATTTCCACGC	148
D	911	caactctcagccagagatgcacaaagtctgtgcagcaactgtctaaagagaacatcagcagctg	970
Q	1490	CAACTGTGAGGCGCTTCACCGGACAAATACACACTGTGCTCGCGGACAACTACAGGCATG	154
D	971	ctctctgtgacctactcgggactgtatctgcacagatcatgaactccaactacgttagactcag	1033
Q	1550	TCCTGGCTCTCATGCTGTGCATGATGTGGTTGTGATGATGACACCCCAACTATGTGACTCCAA	160
D	1031	cagc -ct -cagcgttg - - -caccaatgtgtgactcagaagaacaggcgaatgactctga	108
Q	1610	CCCCACGGGCATCTGTGTTCTCTCCCTGTGTCAATTGTCTGTGGCATGTGGCAATGTGAA	166
D	1085	agactgtctgaatattctgaattctttttaagacaatatctgtctcnaaaatgcaattca	114
Q	1670	AGAGTGTGAAGAGTTCTCTCAGGCACTTCACGGAACCAACCCATGCTCCGAGATGCATCA	172
D	1145	agccttggcgaatggctcagaatgtgaacatgtgtgcacgcagcccccacgtcc	1197
Q	1730	GGCTTTGTGTATGTGCACACATGTGAACAATGTCTCCAAAGGGCCCTCACTTC	1782

RESULT	7	
ID	788419 standard: cDNA: 2568 BP.	
AC	788419;	
DT	01-MAY-1998 (first entry)	
DE	Human glial cell line-derived neurotrophic factor receptor cDNA.	
KW	Human: glial cell line-derived neurotrophic factor; GDNF; receptor	
KW	treatment; dopaminergic nerve cell disorder; Parkinson's disease;	
KW	Alzheimer's disease; amyotrophic lateral sclerosis; diabetes;	
KW	Huntington's disease; glaucoma; retinal degeneration; hearing loss;	
KW	gene therapy; ss.	
KW	Homo sapiens.	
OS	Key	
OS	Location/Qualifiers	

FT	CDS	540..1937
FT		/*tag=
FT		/product=
PN	MO9740152-A1.	GNFNF_receptor
PD	30-OCT-1997.	
PF	15-APR-1997; U06281.	
PR	14-APR-1997; US-837199.	
PR	22-APR-1996; US-015907.	
PR	09-MAY-1996; US-017221.	
PA	(AMGE-.) AMGEN INC.	
PI	Fox GM, Jling S, Wen D;	
DR	WPI: 97-535836/49.	
DR	P-PSDB: W35333.	
PT	glial cell line derived neurotrophic factor receptor - useful to	
PT	treat dopaminergic nerve cell disorders, e.g. Parkinson's and	
PT	Alzheimer's disease	
PS	Claim 17: Pages 91-93; 196pp: English.	
CC	The present sequence encodes the human glial cell line-derived	
CC	neurotrophic factor (GDNF) receptor, which can be used to treat	
CC	dopaminergic nerve cell disorders, e.g. Parkinson's and Alzheimer's	
CC	disease or amyotrophic lateral sclerosis, complications of diabetes	
CC	and Huntington's disease and (optionally in combination with GDNF)	
CC	glaucoma, retinal degeneration and hearing loss caused by injury to	
CC	inner ear sensory neurons. The receptor can also be used to block	
CC	unwanted GDNF activity, analyse GDNF related molecules and	
CC	stabilise GDNF in pharmaceutical formulations. Receptor expression	
CC	cells, preferably transfected ex vivo, can be used similarly to	
CC	implantation, and the use of the receptor cDNA in gene therapy is	
CC	also contemplated. Probes based on the cDNA can be used to detect	
CC	GDNF responsive cells and tissues, e.g. to identify patients who	
CC	would benefit from GDNF therapy, and abnormalities in receptor	
CC	expression, and to isolate molecules that form a complex with the	
CC	cDNA or are homologous/cross-reactive with the cDNA. Anti-receptor	
CC	antibodies, oligonucleotides derived from the cDNA and animal	
CC	models that overexpress the receptor can be used to study the	
CC	biological function of GDNF. knockout transgenic animals can be	
CC	used to detect GDNF dependent neurons or processes and the antibody	
CC	can be used in immunassays for the receptor. The receptor binds	
CC	GDNF specifically and with high affinity, acting as part of a	
CC	complex that mediates/enhances signal transduction by GDNF, i.e.	
CC	increasing dopamine uptake in dopaminergic cells.	
SQ	Sequence 2568 BP: 631 A; 662 C; 625 G; 607 T;	
Query Match	9.5%; Score 210; DB 38; Length 2568;	
Best Local Similarity	65.5%; Pred. No. 1.16e-129;	
Matches	571; Conservative 0; Mismatches 289; Indels 12;	
Db	740 gcccaagatgagtcgcgcagcgcatatgtaggacctgaagaagtcgctctacacacg	
Qy	890 GGGCCATTAAAGATGCGCAGGACACCCCTGGAGGCTTTGGAGAAACCCCTTATGACCT	
Db	800 cgcctgcaagccgggfatgaagaaggaagaagacatgcgcgcgcatcttgagagatg	
Qy	950 CCGCTGCAACGGGGGATGAAGAAGAGCTGCAGTGTCTGCAGATCTACTGGAGATCCA	
Db	860 ccagagccctg-cag--ggaatgatcgtctggagatccccaatgaaccagcttaacag	
Qy	1010 TCGGGGGCTGACAGAGGGTGAAGAGTTCATGAAGCTTCCCTATGAOCTGTGACTC	
Db	917 cagatgtcagatatatcccggttggtcccatcatcatcagatgttttcagcaagtga	
Qy	1070 GCGCCCTCTCGAGACATCTTAGGCTCGCTTCATCTCTCAGGAGACAGGACAGCCGGC	
Db	977 ggcacatcccaaaaggaaacaactgctctggaatgcagcgaagagcctcaactgcagacat	
Qy	1130 GGTCTATACCAAAAGAACACCTGCTGTGATCCCGCAAGGCCCTCCAACTGAAAGACAA	
Db	1037 ttgcaagaagatcaggtcggtgcttaccaccgcgtga-cacacagcg-tgtcaac-ga	
Qy	1190 CTCGAAGAACTTCGCTCCTCTTATATCTCCATCTGCAACCGTGAGATCTCTCCACCGA	
Db	1094 tgcctgcaaccgcgcgcgaagtgcacaagaagccctccgcgagctctcttgacaagtcgcgcg	

QY 1250 ACGCTGCAACCGCGCAGTGCACAGGCTCTGGCCAGTCTTTGACCTGTGCCAG 1309
DB 1154 caagcacagcgaagaaagcctctctgtctccgagacatcgctccacagagagag 1213
QY 1310 CGAGTATACCTACCGCATGCTCTCTGCTCCTGTCAGGACCAAGGAGTGTGAGCGCG 1369
DB 1214 ggcacagacacatcgtctgtctgtctctatgaagaagagagagagagagagagag 1273
QY 1370 CCGGCAACCATCTCCGCGCACTGTCTCTATGAGAGACAGAGAGAGAGAGAGAGAGAG 1429
DB 1274 ttgcagagagctctcgaagagaaattacatctgcagatctgcgcttgcgagatcttttac 1333
QY 1430 CCTGCGCAGCGCTGTCTCTACAGACACACTGTGCGGTCGCCAGCTGAGATTTCCAGCGC 1489
DB 1334 caattgcagcagcagagatcaagctgtctagacagctgtctaaagaaactcgcgtgactg 1393
QY 1490 CAACCTGTGACCTCTCTACCGGACATGACAGCTGTCTCGGACAACTACAGGCGATG 1549
DB 1394 cctctcgcctacacgcgagcttatgtgacagctcagcccccaactacatagactccag 1453
QY 1550 TCTGGGCTCTATGCTGTGCGCATGATGGCTTGATGATGACCAACTATGTGAGACTCCA 1609
DB 1454 tagc-ct--ca--gtg--tggcccaatggtgtgactgcagcaacagtgaggaaacgactaga 1507
QY 1610 CCCACAGCGGCATCGTGTGTCTCCTGCTGCAATGTGCTGGCAGTGGAACATGAGAGA 1669
DB 1508 agagagctgaattttgaatttcttcaagagacatcagctcgtctaaagatcaatca 1567
QY 1670 AGAGTGTAGAGATCTCTACAGGAGATTCACGAAACCACTGCTCCGGAATGCCATCA 1729
DB 1568 agccttgcagcagctcgcagatgtacccgtgt 1599
QY 1730 GGCCTTTGTAATGCGCACAGATGTCAACATGT 1761

RESULT 8
ID T84980 standard; DNA: 201 BP.
AC T84980:
DE Human EST-derived sequence yeb3h05.r1 fragment.
KW Glial cell derived neurotrophic factor receptor alpha; GDNFR alpha;
KW GDNF; human; kidney disease; glomerulonephritis; therapy; EST;
KW expressed sequence tag; ss.
OS Homo sapiens.
PN MO9733912-A2.
PD 18-SEP-1997.
PF 13-MAR-1997; U04363.
PR 14-MAR-1996; US-618236.
PR 14-MAR-1996; US-615902.
PA (GETH) GENENTECH INC.
PI Klein RD, Moore MM, Rosenthal A, Ryan AM;
DR WPI: 97-470819/43.
PT Isolated glial cell derived neurotrophic factor receptor alpha -
PT useful to develop products to diagnose and treat associated
PT disorders, particularly enteric nervous system or kidney disorders
PS Example 1: Page 61: 100pp: English.
CC This DNA sequence comprises a fragment of a human EST-derived
CC sequence designated yeb3h05.r1 (see T84978). It can be used as
CC a probe to identify glial cell derived neurotrophic factor receptor
CC (GDNFR) sequences, including human variants. The invention relates
CC to novel uses of GDNF and its receptor. In particular, it relates
CC to rat GDNFR alpha (see W27327), its variants and soluble derivatives
CC (extracellular domain), chimeric GDNFR alpha and antibodies which
CC bind to the GDNFR alpha, including agonist and neutralizing
CC antibodies, as well as various uses for these molecules. It also
CC relates to assay systems for detecting ligands to GDNFR alpha,
CC systems for studying the physiological role of GDNF, diagnostic
CC techniques for identifying GDNF-related conditions, methods for
CC identifying molecules homologous to GDNFR alpha, and claimed
CC methods for the treatment of GDNF-related and GDNFR alpha-related
CC conditions, particularly kidney disease associated with
CC glomerulonephritis and enteric nervous system related disorders.
CC Transgenic and knockout animals are also claimed.

SQ Sequence 201 BP; 41 A; 78 C; 46 G; 36 T;
Query Match 7.9%; Score 175; DB 37; Length 201;
Best Local Similarity 94.0%; Pred. No. 8.03e-104;
Matches 187; Conservative 0; Mismatches 12; Indels 0; Gap
DB 1 gcaacccatcgtctgaagcgcgcgaagcgcgcgaacccgaaatgaacagcagcgcgcgc 60
QY 1144 GCAACCACTGCTGTGATGCGCGCAAGGCTGCAACCTGATGACACTGCAAGAGCTTC 1203
DB 61 gctctctacatctccatctgcaacgcgagatctgcgccagagcgctcgaacgcgc 120
QY 1204 GCTCTCTTATCTCATCTGCAACCGTAGATCTCTCCACCGAAGCTGCAACCGCC 1263
DB 121 gcaagtgcccaagagcctcgcgcagctgtcttgcacggggtgcgcagagatcaactacc 180
QY 1264 GCAAGTGCACAGGCTGTGCGCATGCTTTGACGCTGTGCCAGGAGTATACCTACC 1323
DB 181 gcatgctctctgctcctg 199
QY 1324 GCATGCTCTCTGCTCCTG 1342

RESULT 9
ID T84981 standard; DNA: 201 BP.
AC T84981:
DE Human EST-derived sequence y170a10.r1 fragment.
KW Glial cell derived neurotrophic factor receptor alpha; GDNFR alpha;
KW GDNF; human; kidney disease; glomerulonephritis; therapy; EST;
KW expressed sequence tag; ss.
OS Homo sapiens.
PN MO9733912-A2.
PD 18-SEP-1997.
PF 13-MAR-1997; U04363.
PR 14-MAR-1996; US-618236.
PR 14-MAR-1996; US-615902.
PA (GETH) GENENTECH INC.
PI Klein RD, Moore MM, Rosenthal A, Ryan AM;
DR WPI: 97-470819/43.
PT Isolated glial cell derived neurotrophic factor receptor alpha -
PT useful to develop products to diagnose and treat associated
PT disorders, particularly enteric nervous system or kidney disorders
PS Example 1: Page 61: 100pp: English.
CC This DNA sequence comprises a fragment of a human EST-derived
CC sequence designated y170a10.r1 (see T84979). It can be used as
CC a probe to identify glial cell derived neurotrophic factor receptor
CC (GDNFR) sequences, including human variants. The invention relates
CC to novel uses of GDNF and its receptor. In particular, it relates
CC to rat GDNFR alpha (see W27327), its variants and soluble derivatives
CC (extracellular domain), chimeric GDNFR alpha and antibodies which
CC bind to the GDNFR alpha, including agonist and neutralizing
CC antibodies, as well as various uses for these molecules. It also
CC relates to assay systems for detecting ligands to GDNFR alpha,
CC systems for studying the physiological role of GDNF, diagnostic
CC techniques for identifying GDNF-related conditions, methods for
CC identifying molecules homologous to GDNFR alpha, and claimed
CC methods for the treatment of GDNF-related and GDNFR alpha-related
CC conditions, particularly kidney disease associated with
CC glomerulonephritis and enteric nervous system related disorders.
CC Transgenic and knockout animals are also claimed.
SQ Sequence 201 BP; 41 A; 78 C; 46 G; 36 T;
Query Match 7.9%; Score 175; DB 37; Length 201;
Best Local Similarity 94.0%; Pred. No. 8.03e-104;
Matches 187; Conservative 0; Mismatches 12; Indels 0; Gap
DB 1 gcaacccatcgtctgaagcgcgcgaagcgcgcgaacccgaaatgaacagcagcgcgcgc 60
QY 1144 GCAACCACTGCTGTGATGCGCGCAAGGCTGCAACCTGATGACACTGCAAGAGCTTC 1203
DB 61 gctctctacatctccatctgcaacgcgagatctgcgccagagcgctcgaacgcgc 120
QY 1204 GCTCTCTTATCTCATCTGCAACCGTAGATCTCTCCACCGAAGCTGCAACCGCC 1263
DB 121 gcaagtgcccaagagcctcgcgcagctgtcttgcacggggtgcgcagagatcaactacc 180
QY 1264 GCAAGTGCACAGGCTGTGCGCATGCTTTGACGCTGTGCCAGGAGTATACCTACC 1323
DB 181 gcatgctctctgctcctg 199
QY 1324 GCATGCTCTCTGCTCCTG 1342

Query Match	Best Local Similarity	Matches	Score	DB	Length
84	catccccaagaaggaacaactgctgatacagcgaagagcctgcaacatcgacacattg	420	Conservative	0	Mismatches 200; Indels 9; Gaps

QY	1133	CAGTACCAAAGACACACACTGCTCGATGCGCGAAGGCGCTGCACCTGATGACACTG	1142
Db	144	caaggaagtagcaagtcgagcgatcatcaacccccgtgca-ccaccagcg-tgttcaac-gatyl	200
QY	1193	CAGAAGAGTGTGCTCTCTATTATATCTCATATCTCAACACGTGATCTCTCCACACGAAAG	1242
Db	201	ctgcaacccgcccgaagtagccacaagaagcccttcggcaggttcttttgcaaggtcccgagaa	257
QY	1233	CTGCACACGCCGCAAGTGCACCAAGGCTCTGGCCCGCATGTTTGACCGTGTGCTCAATG	1292
Db	261	gcacagctcaggaatgtctctcttcgcccctgcgcggagacatgcgctcacaagaagcagaa	317
QY	1313	GATATACCTACCGCATGCTCTTCTGCTCTCTATGAGACACAGGATGTGCTGACGTCGCGC	1362
Db	321	acagaccatcgctgcctctgtgctctcctatgaagaagagagaaagcccaactgtttgaatt	380
QY	1373	GCAAAACATCTCTGCCAGTGTGCTCTATGAGACCAAGGAAGGCCCACTGGCTGGACCT	1432
Db	381	gcaggaactctctgcaagaagcaatatactctgcagatctgcgctctcggaattttttacaa	440
QY	1433	GCGCAGCGCTGTGTGTGTACACACCACCTGTGCGCGTCCGACATGCGAGATTTCACGCCAA	1492
Db	441	ctgcgcagccagagatgcacagatgcctcagcagctgtctcaagaagaaactacgcctgactgct	500
QY	1493	CTGTGACGCTCTCTACCGGCAATACCAAGCTGTCTCGCGCAACTACCAAGCATGTGCT	1552
Db	501	ccctgcctactctcggagctcttttgcaacagtcatacgaaccccaactacataagactcagtag	560
QY	1553	GGGCGCTCATATGCTGGCATGATTGGTTGATATGACACCCACACTATGTGAGCTCCACACC	1612
Db	561	c-ct--gtg-tggcccactgtgtgtgactgcagcaacagtgaggacgacctagaaga	614
QY	1613	CACGGCGATCTGTGTGTCTCTCCCTGTGCAATTGTCTGTGGCACTGGGAACATGGAAGA	1672
Db	615	gtgtcttgaaatttttgattcttctcaaggacaatacatgtctctaaaatgcaattcaagc	674
QY	1673	GTTGTAGAAAGTCTCTCAGGACCTTCACGGAAACCCCATCTCCCGAATGCCATTTCAGGC	1732
Db	675	ctttgcgaatgctcgcagatgcagcgt 703	
QY	1733	CTTTGTATATGCGACAGATGTGAACATGT 1761	
RESULT	11		
ID	V00247	standard; cDNA; 1682 BP.	
AC	V00247;		
DT	21-MAY-1998	(first entry)	
DE	Human Ret. ligand retL cDNA.		
KM	Ret. ligand; RetL; nerve cell; receptor; signal transduction; human;		
KM	cell growth; renal cell; nerve cell; renal failure; nephritis;		
KM	kidney transplant; toxic injury; hypoxic injury;		
KM	neurodegeneration; motor neurone disease; multiple sclerosis;		
KM	infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;		
KM	cranial nerve injury; spinal cord injury; Down's syndrome;		
KM	cerebral palsy; Lyme disease; muscular dystrophy;		
KM	myasthenia gravis; tumour; therapy; ss.		
OS	Homo sapiens.		
Key	location/Qualifiers		
FT	CDS	118..1500	
FT		/tag- a	
PN	MO9744356-A2.		
PD	27-NOV-1997.		
PR	07-MAY-1997; U07726.		
PR	10-APR-1997; US-017427.		
PR	08-MAY-1996; US-017427.		
PR	07-JUN-1996; US-019300.		
PR	16-JUL-1996; US-021859.		
PA	(BioL) BIOGEN INC.		
PI	Cate RL, Hession C, Santicola-Nedel M;		
DR	WPI: 98-018431/02.		
DR	P-PSDS: W37459.		
PT	New nucleic acid encoding ret receptor ligands and related proteins		

PT - vectors, transformed cells and antibodies, used for promoting cell
 PT growth and improving survival of injured cells, especially renal or
 PT nerve cells
 PS Claim 1: Page 62-64: 113bp: English.
 CC This sequence comprises cDNA coding for human Ret ligand (Retl).
 CC Retl (see W37459), a key component of the Ret signaling pathway.
 CC It was deduced from 2 clones isolated from human foetal kidney.
 CC cDNA using primers based on a partial human retl cDNA (see
 CC V00246). Rat retl and mouse and human retl2 and retl3 sequences
 CC have also been identified (see V00245 and V00248-51). The human
 CC retl cDNA is 88.28 identical to rat retl cDNA. Vectors
 CC containing retl DNA and prokaryotic or eukaryotic host cells
 CC transformed or transfected with these vectors are claimed, as well
 CC as a method for production of Retl. Its soluble variants and
 CC fusion proteins with a toxin, imageable compound or radionuclide.
 CC Retl, optionally when expressed from vectors in vivo, is used to
 CC promote growth of new tissue and survival of damaged tissue,
 CC particularly kidney or neural tissue. Typical applications are in
 CC renal failure, nephritis, kidney transplants, toxic or hypoxic
 CC injury, neurodegeneration, motor neurone disease, multiple
 CC sclerosis, bacterial, viral or prion infections (e.g. meningitis,
 CC myelopathy associated with HIV or Creutzfeldt-Jakob disease),
 CC cranial nerve or spinal cord injury, developmental disorders such
 CC as Down's syndrome and cerebral palsy, or conditions involving the
 CC peripheral nervous system (Lyme disease, muscular dystrophy and
 CC peripheral neuropathy). Fusion proteins are used to deliver toxins
 CC etc. to Ret-expressing cells, especially tumours.
 SO Sequence 1682 BP: 417 A; 461 C; 433 G; 371 T;

Query Match 7.5%; Score 166; DB 39; Length 1682;
 Best Local Similarity 66.8%; Pred. No. 3,22e-97;
 Matches 420; Conservative 0; Mismatches 200; Indels 9; Gaps 7;

Db 543 catcccaaaagggaacacacgctgctgagcaggaagcctgcgaactgcagcattg 602
 Qy 1133 CAGTACCAAAAGCAACACCTCCGATGCGCGCAAGGCTCGCACTGATGACCACTG 1192
 Db 603 caaagaatagcagcgcgtacacaccgcgtgca-cacccaagc-ggtccaac-gatgt 659
 Qy 1193 CAGAAGCTTCGCTCTTATATCTCATCTGCAACCGTAGATCTCTCCACGGAACG 1252
 Db 660 ctgcgaacgcgcgaagctgcaaaagcctcgcgcagcttcttgcaaggtccgcgcaaa 719
 Qy 1253 CTGCAACCGCGCGCAAGTGCCACAAGGCTCGCCAGCTTTTACGCTGAGCCACGA 1312
 Db 720 gcaacagctaggaatgctcttctcctcgcgcggaacatgcgcgcagcagcgagggc 779
 Qy 1313 GTATACCTACCGCATGCTCTTCTCTCTGACAGGACCAAGCATGCTGAGCGTCCG 1372
 Db 780 acagacacatgctgctgtgctcctctatgaagagaggaagcacaactgttgaattt 839
 Qy 1373 GCAAAACCATCTGCGCCAGTTCTCTATGAGAGACAGAGAACCCCACTGCGACT 1432
 Db 840 gcaaggaactcctgcaagaacgaatcatctgcagatcctgccttgcggaatttttacc 899
 Qy 1433 GCGGAGCTGTGTGCTGACAGACACTGTGCGGCTCCGACTGCAATTTCCACGCCAA 1492
 Db 900 ctgcgaacgcgcgaagctgctgcaagcagctgtctaagaagaacacagctgctcct 959
 Qy 1493 CTGTGAGGCTCTTACCGGGAATCACCACTGTCTGCGGACCACTACCGAGCATGTCT 1552
 Db 960 cctgcgaactcgcgggcttatgtgacacagtcatacccccacaatacagaactcagtag 1019
 Qy 1553 GGGCTCTATGCTGCGCATGATGGGTTGATATACACCCCACTATGTGACTCCAAACC 1612
 Db 1020 c-ct--gtg-tggccccatggtgtgacagcaaacagctggaagcactagaaga 1073
 Qy 1613 CACGGGATGCTGTGTCTCTGCTGCAATTTGTGTCGAGTGGGAACATGAGAAGA 1672
 Db 1074 gtgtgtgaaatttttgaaatttctcaagaagaacaatacatttcttaaaatgaattcagc 1133
 Qy 1673 GTGTGAGAAAGTTCTCTCAGGGAATTACAGGAATCCCATGCTCGGAAATGCCATTGAGCG 1732

Db 1134 ctctggcaatgctccgcatgacgctgt 1162
 Qy 1733 CTTTGGTAATGGCAGATGTGAAATGCT 1761

RESULT 12
 ID T84977 standard; cDNA: 840 BP.
 AC T84977;
 DT 27-APR-1998 (first entry)
 DE Mouse GDNF alpha clone 26 3' end.
 KM Glial cell derived neurotrophic factor receptor alpha: GDNFR alpha:
 KW GDNF: mouse; kidney disease: glomerulonephritis; therapy: ss.
 OS Mus musculus.
 PN M09733912-A2.
 PD 18-SEP-1997.
 PF 13-MAR-1997: U04363.
 PR 14-MAR-1996: US-618236.
 PR 14-MAR-1996: US-615902.
 PA (GETH) GENENTECH INC.
 PI Klein RD, Moore MW, Rosenthal A, Ryan AM;
 DR WPI: 97-470819/43.
 PT Isolated glial cell derived neurotrophic factor receptor alpha
 PT useful to develop products to diagnose and treat associated
 PT disorders, particularly enteric nervous system or kidney disorders.
 PS Example 1: Page 60-61; 100p: English.
 CC This cDNA sequence comprises the 3' end of mouse full-length
 CC glial cell derived neurotrophic factor receptor alpha (GDNFR alpha)
 CC (see W27327) clone 26; the 5' end of the clone is given in
 CC T84978. Clone 26 was isolated from a mouse cDNA library using
 CC rat GDNFR alpha cDNA (see T84975) as probe. The invention relates
 CC to novel uses of GDNF and its receptor. In particular, it relates
 CC to native rat GDNFR alpha (see W27327), its variants and soluble
 CC derivatives (extracellular domain), chimeric GDNFR alpha and
 CC antibodies which bind to the GDNFR alpha, including agonist and
 CC neutralising antibodies, as well as various uses for these
 CC molecules. It also relates to assay systems for detecting ligands
 CC to GDNFR alpha, systems for studying the physiological role of
 CC GDNF, diagnostic techniques for identifying GDNF-related conditions,
 CC methods for identifying molecules homologous to GDNFR alpha, and
 CC therapeutic techniques (claimed) for the treatment of GDNF-related
 CC and GDNFR alpha-related conditions, particularly kidney disease,
 CC associated with glomerulonephritis and enteric nervous system
 CC related disorders. Transgenic and knockout animals are also
 CC claimed.
 SO Sequence 840 BP: 205 A; 245 C; 200 G; 190 T;

Query Match 5.6%; Score 125; DB 37; Length 840;
 Best Local Similarity 64.8%; Pred. No. 1.94e-67;
 Matches 339; Conservative 0; Mismatches 178; Indels 6; Gaps 4;

Db 1 cgcgcgaagggcgaacaaagccctcagcagcttcttgacaagttccagcgaagccagc 60
 Qy 1260 CGCGCAAGGCGCCACAAGGCTTGCGCCAGTTCTTTGACGCTGCGCCAGCGATTAAC 1319
 Db 61 tacggatgctcttctgctcctcgcgcggaagctgcctgcacccagagggcgagcagact 120
 Qy 1320 TACCGCATGCTCTTCTGCTCTCTCTGACAGACAGCATGTGCTGAGGCTGCGGCAAC 1379
 Db 121 atcgtccctgtgtctcctatgaagaacgagagggcccaactgctgaattctgcaagac 180
 Qy 1380 ATCTCTCCCGAGTGTCTCTATGAGACAAGAGAACCCCAACTGCTGACCTGCGCAC 1439
 Db 181 tcttgcaagcaaatatacatctgcagatctgcctgcagagattttttccaactgcag 240
 Qy 1440 CTGTGTGCTACACCAACCTGCTGCGCTCCGCTGCGCATGCGCATTTCCACGCACTGTGA 1499
 Db 241 ccagagtcgaaggtctgcagcaactgcttaagaagaacagcagactgcctcggcgc 300
 Qy 1500 GCCTCTACCGGACATACACAGCTCTCTGCGGACAACTACACAGCATGTCTGGGCTTC 1559
 Db 301 tactcggaactgatttggcagcagctacactcctaatacagactcagcagc-ct--c 357
 Qy 1560 TATGCTGCAATGATGGGTTGATATGACACCAACTATGTGACTCAACCCACGAGGC 1619

Mon Mar 15 06:28:33 1999

US-08-866-354-39.rng

Page 11

Search completed: Fri Mar 12 10:08:30 1999
Job time : 454 secs.

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(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Mon Mar 8 14:25:40 1999; MasPar time 16.27 Seconds

457.512 Million cell updates/sec

Tabular output not generated.

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Description: (1-460) From US08866354.pep
Perfect Score: 3343
Sequence: 1 MLVPSHYPDETIRLASS.....RRASALTALPLIMLTAL 460
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Scoring table: PAM 150
Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 08
Listing first 45 summaries

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Database:
a-geneseq32
1:part1 2:part3 3:part4 4:part4 5:part5 6:part5 7:part5
8:part8 9:part9 10:part10 11:part11 12:part11 13:part11
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29
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Statistics: Mean 34.963; Variance 141.378; scale 0.247

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	3131	93.7	464	28	W37460	Human Ret ligand RetL	0.00e+00
2	1560	46.7	488	28	W35334	Rat glial cell line-d	1.20e-14
3	1560	46.7	488	28	W37457	Rat Ret ligand RetL	1.20e-14
4	1560	46.7	468	27	W27327	Rat glial cell derive	1.20e-14
5	1523	45.6	465	28	W35333	Human glial cell line	9.42e-14
6	1501	44.9	460	28	W37459	Human Ret ligand RetL	1.94e-14
7	1144	34.2	346	28	W37458	Human Ret ligand RetL	5.39e-16
8	777	23.2	397	28	W37461	Human Ret ligand RetL	7.39e-16
9	750	22.4	346	28	W37465	Mouse Ret ligand RetL	4.89e-63
10	711	21.3	400	28	W37463	Mouse Ret ligand RetL	4.61e-59
11	675	20.2	315	28	W37462	Human Ret ligand RetL	2.29e-55
12	103	3.1	1712	1	R24261	Human Ret ligand RetL	4.73e+00
13	98	2.9	179	23	W21646	Masking protein high	1.47e+00
14	92	2.8	550	10	R52831	Gravineine leifroll v1	3.17e+01
15	94	2.8	650	1	R81137	Sequence of human alp	3.17e+01
16	94	2.8	650	1	R81137	Human protein S	2.26e+01
17	84	2.8	4472	26	W22601	Tylectone synthase OR	2.26e+01
18	89	2.7	325	17	R25074	WD-40 domain-contg. P	5.24e+01
19	89	2.7	325	17	R25074	FLAP.	5.24e+01

ID	W37460 standard; Protein: 464 AA.	
AC	W37460;	
DT	21-MAY-1998 (first entry)	
DE	Human Ret ligand RetL2.	
KM	Ret ligand, RetL, RetL2; receptor; signal transduction; human;	
KM	cell growth; renal cell; nerve cell; nerve failure; nephritis;	
KM	kidney transplant; toxic injury; hypoxic injury;	
KM	neurodegeneration; motor neurone disease; multiple sclerosis;	
KM	infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;	
KM	cerebral nerve injury; spinal cord injury; Down's syndrome;	
KM	cerebral palsy; Lyme disease; muscular dystrophy;	
KM	myasthenia gravis; tumour; therapy.	
OS	Homo sapiens.	
PN	M09744356-A2.	
PD	27-NOV-1997.	
PF	07-MAY-1997; U07726.	
PR	10-APR-1997; US-017427.	
PR	08-MAY-1996; US-017427.	
PR	07-JUN-1996; US-019300.	
PR	16-JUL-1996; US-021859.	
PA	(BIOC) BIOGEN INC.	
PI	Cate RL, Hession C, Santicola-Nedel M;	
DR	WPI: 98-018431/02.	
DR	N-PDSB: V00248.	
PT	New nucleic acid encoding ret receptor ligands and related proteins	
PT	- vectors, transformed cells and antibodies, used for promoting cell	
PT	growth and improving survival of injured cells, especially renal n	
PT	erve cells	
PS	Claim 2; Page 69-70; 113pp; English.	
CC	This amino acid sequence comprises human Ret ligand (RetL) RetL2,	
CC	deduced from a cDNA clone (see V00248) isolated from a human foetal	
CC	liver library. Rat and human RetL, and human and mouse Human	
CC	sequences (see W37457-59 and W37461-63) are also claimed. Human	
CC	RetL2 is 49.1% identical to human RetL protein. RetL is a	
CC	key component of the Ret signalling pathway that specifically	
CC	interacts with Ret receptor protein, triggering Ret dimerisation	
CC	and/or autophosphorylation of the Ret tyrosine kinase domain.	
CC	Vectors containing RetL2 DNA and prokaryotic or eukaryotic host	
CC	cells transformed or transfected with these vectors are claimed, as	
CC	well as a method for production of RetL2, its soluble variants and	
CC	fusion proteins with a toxin, imageable compound or radionuclide.	

[illegible]

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ORGANISM      Streptomyces griseus
DATE          26-May-1994 #sequence_revision 26-May-1994 #text_change
              09-Sep-1997
ACCESSIONS    A47096
REFERENCE      Ueda, K.; Miyake, K.; Horiouchi, S.; Beppu, T.
              J. Bacteriol. (1993) 175:2006-2016
              A gene cluster involved in aerial mycelium formation in
              Streptomyces griseus encodes proteins similar to the
              response regulators of two-component regulatory systems and
              membrane translocators.
#accession    A47096
#status       preliminary
#molecule_type DNA
#residues     1-201 #label UED
#cross-references GB:DJ613; NID:g303909; PID:d1003289; PID:g303913
KEYWORDS      DNA binding; phosphoprotein
FEATURES
  54
SUMMARY        #binding_site phosphate (Asp) (covalent) #status
                predicted
                #length 201 #molecular_weight 21329 #checksum 9963

Query Match    2.9%: Score 96; DB 2; Length 201;
Best Local Similarity 34.5%: Pred. No. 9.15e-01;
Matches 10; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

Db 36 AIRALGSPDVLITDIDCPGALDVIDE 64
      ::|||:::||||:|||||:|
Qy 55 TLROCLAGRDNTMLANKECALVEIQE 83

RESULT 5
ENTRY   S72723 #type complete
TITLE   dipeptide transport protein precursor homolog dcIAE -
         Mycobacterium leprae
ALTERNATE_NAMES B1177_C1_166 protein
ORGANISM #formal_name Mycobacterium leprae
DATE      19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change

ACCESSIONS S72723
REFERENCE   S72693
           Smith, D.R.; Robison, K.
           Submitted to the EMBL Data Library, November 1993
           Mycobacterium leprae cosmid B1177.
           #accession S72723
           #status preliminary
           #molecule_type DNA
           #residues 1-344 #label SMI
           #cross-references EMBL:U00011; NID:g466807; PID:g466812
GENETICS
#gene      dcIAE
#start_codon GCG
SUMMARY    #length 344 #molecular_weight 36103 #checksum 5536

Query Match    2.9%: Score 97; DB 2; Length 344;
Best Local Similarity 37.2%: Pred. No. 6.66e-01;
Matches 16; Conservative 11; Mismatches 14; Indels 2;

Db 84 HSGOLRAHRLAVGSHRAADICAAAGCCGPRPALAC-TPRD 125
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy 23 QGSELHGMRPOYDCVRANELICAA-ESNCSSRYTLRQCLAGRD 64

RESULT 6
ENTRY   B70518 #type complete
TITLE   probable clinA - Mycobacterium tuberculosis (strain H37RV)
ORGANISM #formal_name Mycobacterium tuberculosis
DATE      17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change

ACCESSIONS B70518
REFERENCE   A70500
           Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher,
           #authors

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Query Match 95.6%; Score 3196; DB 1; Length 463;
 Best Local Similarity 96.9%; Pred. No. 0.00e+00;
 Matches 438; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

DB 12 FLDETLASLSPSSLOGSELHGMRPVDCVRANELCAAESNCSSRYRTLROCLAGDRNT 71
 : |||||
 OY 8 YPEETLRLSLASPSLOGSELHGMRPVDCVRANELCAAESNCSSRYRTLROCLAGDRNT 67
 |||||

DB 72 MLANKECOALAEVLOESPLDYDCRCKRGMKKELOCIQIYWSIHGLTEGEFEYEAPEPV 131
 |||||
 OY 68 MLANKECOALAEVLOESPLDYDCRCKRGMKKELOCIQIYWSIHGLTEGEFEYEAPEPV 127
 |||||

DB 132 TSRLSDIFRLASIFSGTGADPVYSAKSNHCLDAKACNLNDCKKLRSSYISICNREISP 191
 |||||
 OY 128 TSRLSDIFRLASIFSGTGADPVYSAKSNHCLDAKACNLNDCKKLRSSYISICNREISP 187
 |||||

DB 192 TERCNRKCKHKLROFEDVPSEYTYRMLFCSCODACAERRRQTIIPSCSYEDKEXPNC 251
 |||||
 Y 188 TERCNRKCKHKLROFEDVPSEYTYRMLFCSCODACAERRRQTIIPSCSYEDKEXPNC 247
 |||||

DB 252 LDRSLCRTLDRSLADFHANCRASTRITSCPADNYOACLSYAGMIGFDMTPNYVD 311
 |||||
 OY 248 LDRSLCRTLDRSLADFHANCRASTRITSCPADNYOACLSYAGMIGFDMTPNYVD 307
 |||||

DB 312 SNETGIVSPWCMCRSGSGNMECEKFLDFTENPCLRNALIOAFNGTDVNMSPKGPTEF 371
 |||||
 OY 308 SNETGIVSPWCMCRSGSGNMECEKFLDFTENPCLRNALIOAFNGTDVNMSPKGPTEF 367
 |||||

DB 372 ATQAPRVEKTPSLPDLSDSTSLGTSYITTCISIOEGLKANKSKELSMCFELTTNISP 431
 |||||
 OY 368 ATQAPRVEKTPSLPDLSDSTSLGTSYITTCISIOEGLKANKSKELSMCFELTTNISP 427
 |||||

DB 432 GSKKVIKLYSGSRARLSTALTPLLMTLTA 463
 |||||
 OY 428 GSKKVIKLYSGSRARLSTALTPLLMTLTA 459
 |||||

RESULT 2
 ID NRTN_HUMAN STANDARD: PRT: 464 AA.
 AC 000451:
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE NEURTURIN RECEPTOR ALPHA PRECURSOR (NTRN-ALPHA) (TGFB-
 BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 2) (GDNF RECEPTOR BETA)
 DE (GDNFR-BETA)
 GN GFR2 OR GDNFRB OR TNFR2.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97325791.
 RA BALCH R.H., TANSEY M.G., GOLDEN J.P., CREEDON D.J.,
 RA HEUCKEROTH R.O., KECK C.L., ZIMONIC D.B., POPESCU N.C.,
 RA JOHNSON E.M. JR., MILBRANDT J.;
 RA NEURON 18:793-802(1997).
 CC -1- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NRTN-INDUCED
 AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR. ALSO ABLE
 TO MEDATE GDNF SIGNALING THROUGH THE RET TYROSINE KINASE
 RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
 SIMILARITY).
 CC -1- ALTERNATIVE PRODUCTS: A SHORT FORM IS PRODUCED BY ALTERNATIVE
 SPLICING IN BOTH BRAIN AND PLACENTA.
 CC -1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.
 DR EMBL: AF002700; G2145080; -.
 DR MIM: 601956; -.
 KW RECEPTOR; GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL;
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 444 TGF-BETA RELATED NEUROTROPHIC FACTOR

FT PROPEP 445 464 RECEPTOR 2.
 FT CARBOHYD 52 52 HYDROPHOBIC, REMOVED DURING MATURATION
 FT CARBOHYD 357 357 (POTENTIAL).
 FT CARBOHYD 413 413 POTENTIAL.
 FT LIPID 444 444 POTENTIAL.
 FT VARSPLEIC 14 146 GPI-ANCHOR (POTENTIAL).
 SO SEQUENCE 464 AA; 51558 MW; 3C74BBFB CRC32;

Query Match 93.3%; Score 3120; DB 1; Length 464;
 Best Local Similarity 94.0%; Pred. No. 0.00e+00;
 Matches 426; Conservative 17; Mismatches 10; Indels 0; Gaps 0;

DB 12 FLDETLASLSPSSLOGSELHGMRPVDCVRANELCAAESNCSSRYRTLROCLAGDRNT 71
 : |||||
 OY 8 YPEETLRLSLASPSLOGSELHGMRPVDCVRANELCAAESNCSSRYRTLROCLAGDRNT 67
 |||||

DB 72 MLANKECOALAEVLOESPLDYDCRCKRGMKKELOCIQIYWSIHGLTEGEFEYEAPEPV 131
 |||||
 OY 68 MLANKECOALAEVLOESPLDYDCRCKRGMKKELOCIQIYWSIHGLTEGEFEYEAPEPV 127
 |||||

DB 132 TSRLSDIFRLASIFSGTGADPVYSAKSNHCLDAKACNLNDCKKLRSSYISICNREISP 191
 |||||
 OY 128 TSRLSDIFRLASIFSGTGADPVYSAKSNHCLDAKACNLNDCKKLRSSYISICNREISP 187
 |||||

DB 192 TERCNRKCKHKLROFEDVPSEYTYRMLFCSCODACAERRRQTIIPSCSYEDKEXPNC 251
 |||||
 OY 188 TERCNRKCKHKLROFEDVPSEYTYRMLFCSCODACAERRRQTIIPSCSYEDKEXPNC 247
 |||||

DB 252 LDRGVCRTHLDRSLADFHANCRASTRITSCPADNYOACLSYAGMIGFDMTPNYVD 311
 |||||
 OY 248 LDRSLCRTLDRSLADFHANCRASTRITSCPADNYOACLSYAGMIGFDMTPNYVD 307
 |||||

DB 312 SNETGIVSPWCMCRSGSGNMECEKFLDFTENPCLRNALIOAFNGTDVNMSPKGPTEF 371
 |||||
 OY 308 SNETGIVSPWCMCRSGSGNMECEKFLDFTENPCLRNALIOAFNGTDVNMSPKGPTEF 367
 |||||

DB 372 ATQAPRVEKTPSLPDLSDSTSLGTSYITTCISIOEGLKANKSKELSMCFELTTNISP 431
 |||||
 OY 368 ATQAPRVEKTPSLPDLSDSTSLGTSYITTCISIOEGLKANKSKELSMCFELTTNISP 427
 |||||

DB 432 GSKKVIKLYSGSRARLSTALTPLLMTLTA 464
 |||||
 OY 428 GSKKVIKLYSGSRARLSTALTPLLMTLTA 460
 |||||

RESULT 3
 ID NRTN_CHICK STANDARD: PRT: 465 AA.
 AC 013157:
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE NEURTURIN RECEPTOR ALPHA PRECURSOR (NTRN-ALPHA) (GDNF
 RECEPTOR BETA) (GDNFR-BETA).
 DE GFR2 OR GDNFRB.
 GN GALLUS GALLUS (CHICKEN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;
 OC GALLIFORMES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN.
 RA BU-BELLO A., AND J., PINON L.G.P., HORTON A., THOMPSON J.,
 RA ROSENTHAL A., CHINCHETRU M., BUCHMAN V.L., DAVIES A.M.;
 RL NATURE 387:721-724(1997).
 CC -1- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NRTN-INDUCED
 AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR. ALSO ABLE
 TO MEDATE GDNF SIGNALING THROUGH THE RET TYROSINE KINASE
 RECEPTOR (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.
 CC -1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.
 DR EMBL: U90542; G213805; -.
 DR RECEPTOR; GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL.

FT	SIGNAL	1	21	POTENTIAL.
FT	CHAM	22	445	NEUTRINUM RECEPTOR ALPHA.
FT	PROPER	446	465	HYDROPHOBIC, REMOVED DURING MATURATION (POTENTIAL).
FT	CARBOHYD	355	355	POTENTIAL.
FT	CARBOHYD	387	387	POTENTIAL.
FT	CARBOHYD	412	412	POTENTIAL.
FT	LIPID	445	445	GPI-ANCHOR (POTENTIAL).
SO	SEQUENCE	465 AA:	51908 MW:	5CA073E4 CRC32:
Query Match				
Best Local Similarity		78.2%:	Score 2615:	DB 1; Length 465:
Matches 343:		Conservative 67:	Mismatches 41:	Indels 5; Gaps 3
Db	12	FVDELTLRLAAPPSPGGODLOGMRVPVDCIRANKICAAEGSCSSRYRTLRLOCLAGRDRT	71	
Qy	8	YDELTLRLASPPSLQSGELHGMRPQVDCVANELCAAEENSCSSRYRTLRLOCLAGRDRT	67	
Db	72	MLANECOAALVLOESPLVDCRCRGMKRELOCQVWWSHLGLAESEFEYEAAPYPI	131	
Qy	68	MLANECOAALVLOESPLVDCRCRGMKRELOCQVWWSHLGLAESEFEYEAAPYPI	127	
Db	132	TSRLSDIFRLASIFSGM--DPATNCSNHGCLDAKACNLNDCRKLRSYGISTCSKEISA	189	
Qy	128	TSRLSDIFRLASIFSGITDTPAVSTKSNHCLDAKACNLNDCRKLRSYISICNREISP	187	
Db	190	TEHCSRRKCHKALROFEDNVPESEYTYRLFLSCCKDAQCAEPRDRTVPFCSEYDEKPNC	249	
Qy	188	TERCNRKCHKALROFEDNVPESEYTYRMLFSCSDQACAEPRRDTIPSCYEDKEKPNC	247	
Db	250	LDLRNVCADHLCSRRLADFHANCAOSQSLTSCGDNVYQACLSGYTLLIFDMTPNVYD	309	
Qy	248	LDLRNLCRTHDCRRLADFHANCAASYRTTSCPADVYQACLSGYAGMIGFDMTPNVYD	307	
Db	310	ASTSIITSPKSCSGNLEBECEKFLRDTENPCLRNLAQAFNGDVMLSPPNPSP	369	
Qy	308	SNPFGIVVSPKNCNGSGNMEBECEKFLRDTENPCLRNLAQAFNGDVMNRPKPSLP	367	
Db	370	ITMLPKVEKSPALPDINDSNMTYDTSITTCSTIOEHGRLNKSKEOSLCSYSETOLT	429	
Qy	368	ATQAPRVEKTPSLPDLDLSDTSL-GTSVITTCSTIOEGGLANNKSKELSMCFTE--LTTN	424	
Db	430	TMPDOKTFVDQKAAGSRHRAARILPAVIVLVILKL	465	
Qy	425	ISPGSKVYIKLNSGSSRARLSMALYALPLMLTLAL	460	
RESULT 4				
ID	GNR_RAT	STANDARD:	PRT:	468 AA.
AC	062997:			
DT	01-NOV-1997 (REL. 35, CREATED)			
DT	01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)			
DT	15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)			
DE	GNMF RECEPTOR ALPHA PRECURSOR (GNMF-ALPHA) (GCF-BETA RELATED			
DE	NEUROTROPHIC FACTOR RECEPTOR 1) (RET LIGAND 1).			
GN	GFRA1 OR GDNFRA OR TRNRI OR RETLI.			
OS	RATTUS NORVEGICUS (RAT).			
OC	EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:			
OC	EUMERIA: RODENTIA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-RETINA:			
RX	MEDLINE: 96270513.			
RA	JING S., WEN D., YU Y., HOLST P.L., LDO Y., FANG M., TAMIR R.,			
RA	ANTONIO L., HU 2., CUPPLES R., LOUIS J.-C., HU S., ALTRICK B.W.,			
RA	FOX G.M.,			
RL	CELL 85:113-1124(1996).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-MISTAR: TISSUE-KIDNEY:			
RX	MEDLINE: 97322356.			
RA	SANICOLA M., HESSON C.A., WOLEY D.S., CARMILLO P., EHRENFELS C.,			
RA	WALUS L., ROBINSON S., JAWORSKI G., WEI H., TIZARD R., WHITY A.,			

[illegible]

RESULT	5	STANDARD;	PRT;	468	AA
ID	GDNR-MOUSE				
AC	P97785;				
DT	01-NOV-1997	(REL. 35, CREATED)			
DT	01-NOV-1997	(REL. 35, LAST SEQUENCE UPDATE)			

DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF-BETA RELATED
DE NEUROTROPHIC FACTOR RECEPTOR 1).
GN GFR1 OR GDNFRA OR TRNRI.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN EUTHERIA; RODENTIA.
[1]
RP SEQUENCE FROM N.A.
RC TISSUE-DORSAL ROOT GANGLION;
RA WATRE K;
RL SUBMITTED (FEB-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED
CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR (BY
CC SIMILARITY).
CC -1- SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE THOUGHT TO FORM A COMPLEX
CC WITH THE DISULFIDE-LINKED GDNF DIMER AND WITH 2 MOLECULES OF RET
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.
CC EMBL: AB000800; G1816442; -
DR MCD; MGT:1100842; GFR1.
KM RECEPTOR; GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL.
FT SIGNAL 1 24
FT CHAIN 25 430
FT PROPEP 431 468
FT DOMAIN 362 369
FT CARBOHYD 59 59
FT CARBOHYD 347 347
FT CARBOHYD 406 406
FT LIPID 430 430
SQ SEQUENCE 468 AA; 51782 MW; 6C64C182 CRC32;
Query Match 46.18; Score 1541; DB 1; Length 468;
Best Local Similarity 47.98; Pred. No. 0.00e+00;
Matches 214; Conservative 103; Mismatches 116; Indels 14; Gaps 12;
Db 16 LMSAEVSG-GDRLDVCAKSDQCKECSCTKRYTLRQCVAGKESNLSGLEAKESCS 74
OY 22 LQSEELHGRPOVDVRAVELCAEESCSRYTLRQCLAGRNR-TM--LANK-ECQA 76
Db 75 AMELAKOKSLYCKRCKRKKKCKRRIYMSYOSL-OGNDLDESPYEPVNSRLSDIR 133
OY 77 ALEVLQESPLYDORCKRKKKELQCIQIYMSHGLTGESEFEYASPYEPVNSRLSDIR 136
b 134 AVPELIDVQOYEHLSKNNCLDAKACNLDCTCKRYRSAYITPCTTMS-NEVCNRRK 192
OY 137 LASFEGTGTDPAVSTKSHNCDAKACNLDCKRLRSSYISICNREISPERCNRRC 196
Db 193 HKALRPFEPKPAKSHYGLFCSGRVACTERRRQTIYVCSSEERENCLNLDSCYT 252
OY 197 HKALRPFEPKPAKSHYGLFCSGRVACTERRRQTIYVCSSEERENCLNLDSCYT 256
Db 253 NYICRSRLADFTNCPESRSYCNLCENYADCLAYSLGIGTVMTPNIDSS-S-LSYA 310
OY 257 DHLCRSLADFTNCPESRSYCNLCENYADCLAYSLGIGTVMTPNIDSS-S-LSYA 316
Db 311 PNCDCNSGNDLEDCIKLFNEFKNDTCLENAIOAFNGSDVYTMOPAPVOTTTATTTA 370
OY 317 PNCDCNSGNDLEDCIKLFNEFKNDTCLENAIOAFNGSDVYTMOPAPVOTTTATTTA 375
Db 371 PFKKKPLGPASSENPPIHYVPCANIOAQCLKSVSGSTHCLSDNDYKDGCLAGASS 430
OY 376 -KTPPLPDLDSDTS-LGTSVITCTSTIOEGLKANNKSELSMCTELTINISPSKVIY 433
Db 431 HITTSMAPSPCSGLSLPVWVETALA 457
OY 434 KUNSSSRARLSAALTALPLMLT-LA 459
RESULT 6

ID GDNF CHICK STANDARD: PRT: 469 AA.
AC 013156;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF-BETA RELATED
DE NEUROTROPHIC FACTOR RECEPTOR 1).
GN GFR1 OR GDNFRA.
OS GALUS GALUS (CHICKEN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHA;
RN GALIFORMES.
[1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA BUJ-BELLO A.; ADU J.; PINON L.G.P.; HORTON A.; THOMPSON J.;
RA ROSENTHAL A.; CHINCHETRU M.; BUCHMAN V.L.; DAVIES A.M.;
RL NATURE 387:721-724(1997).
CC -1- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED
CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR (BY
CC SIMILARITY).
CC -1- SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE THOUGHT TO FORM A COMPLEX
CC WITH THE DISULFIDE-LINKED GDNF DIMER AND WITH 2 MOLECULES OF RET
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.
CC EMBL: U90541; G2213803; -
DR RECEPTOR; GLYCOPROTEIN; GPI-ANCHOR; MEMBRANE; SIGNAL.
FT SIGNAL 1 27
FT CHAIN 28 430
FT PROPEP 431 469
FT DOMAIN 361 368
FT CARBOHYD 62 62
FT CARBOHYD 163 163
FT CARBOHYD 346 346
FT CARBOHYD 405 405
FT LIPID 430 430
SQ SEQUENCE 469 AA; 52043 MW; C8D2A1C9 CRC32;
Query Match 45.48; Score 1519; DB 1; Length 469;
Best Local Similarity 50.18; Pred. No. 0.00e+00;
Matches 221; Conservative 99; Mismatches 96; Indels 25; Gaps 17;
Db 29 RIDCVKASDQCKECSCTKRYTLRQCVAGKESNLSGLEAKESCS 88
OY 33 QVDCVRAVELCAEESCSRYTLRQCLAGRD---RTMLANK-ECQALEVLQESPLY 87
Db 89 NCRCRKKKKKCKRRIYMSYOSL-OGNDLDESPYEPVNSRLSDIRLAPYS--VE 144
OY 88 DCRCKRKKKKKCKRRIYMSYOSL-OGNDLDESPYEPVNSRLSDIRLAPYS--VE 144
Db 145 PVL-S-KGNNCDAKACNLDCTCKRFRSAYITPCTTMS-NEICNRRCKHALRFPDKY 202
OY 148 PAVSTKSHNCDAKACNLDCKRLRSSYISICNREISPERCNRRCCHALRQFDRV 207
Db 203 PPKSHYGLFCSGRVACTERRRQTIYVCSSEERENCLNLDSCYT 262
OY 208 PSEYTYRMLFCSCDQCAERROTILPSCSYEDREKENCNLDLSCLTHLCSRLADF 267
Db 263 FTNCPESRSYCNLCENYADCLAYSLGIGTVMTPNIDSS-S-LSYAPNCDCNSGND 320
OY 268 HANCASTRITSCPADYQACLSYAGMIGFDMTPNVDSNPFGIYVSPNCRGSGNM 347
Db 321 IDECRKFLNFPQDWTCLNAIOAFNGSDVYTMOPAPVOTTTATTTASRLKNTGNC 457
OY 328 EEECEKFLADFTNCPESRSYCNLCENYADCLAYSLGIGTVMTPNIDSS-S-LSYA 457
Db 379 TTNEIPTHNDSPACANIOAQKRRKSNESYDTCLNENAIKGNKNTPGVSTS-HISSNN 457
OY 387 STS--LGT-SVITCTSTIOEGL-KANNKSELSMCTE-LTINISGSKKVIYLNKGN 457
Db 438 FA-LPTSFYPTPLMLTIAL 457

FT	SITE	734	736	CLEAVAGE (POTENTIAL).
FT	PROPEP	1575	1577	CLEAVAGE (POTENTIAL).
FT	DOMAIN	1578	1712	POTENTIAL.
FT	DOMAIN	181	213	EGF-LIKE 1.
FT	DOMAIN	391	423	EGF-LIKE 2.
FT	REPEAT	351	604	INTERNAL REPEAT 1.
FT	DOMAIN	618	658	EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT	REPEAT	671	721	INTERNAL REPEAT 2.
FT	DOMAIN	865	906	EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	907	948	EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	949	989	EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	990	1029	EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	1030	1070	EGF-LIKE 8, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	1071	1111	EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	1112	1152	EGF-LIKE 10, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	1153	1193	EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	1194	1235	EGF-LIKE 12, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	1236	1277	EGF-LIKE 13, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	1278	1320	EGF-LIKE 14, CALCIUM-BINDING (POTENTIAL).
FT	REPEAT	1340	1392	INTERNAL REPEAT 3.
FT	DOMAIN	1415	1457	EGF-LIKE 15, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	1458	1498	EGF-LIKE 16, CALCIUM-BINDING (POTENTIAL).
FT	REPEAT	1517	1568	INTERNAL REPEAT 4.
FT	DOMAIN	1612	1652	EGF-LIKE 17.
FT	DOMAIN	1653	1697	EGF-LIKE 18, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	185	195	BY SIMILARITY.
FT	DISULFID	189	201	BY SIMILARITY.
FT	DISULFID	203	212	BY SIMILARITY.
FT	DISULFID	395	405	BY SIMILARITY.
FT	DISULFID	399	411	BY SIMILARITY.
FT	DISULFID	413	422	BY SIMILARITY.
FT	DISULFID	622	633	BY SIMILARITY.
FT	DISULFID	628	642	BY SIMILARITY.
FT	DISULFID	644	657	BY SIMILARITY.
FT	DISULFID	869	881	BY SIMILARITY.
FT	DISULFID	876	890	BY SIMILARITY.
FT	DISULFID	892	905	BY SIMILARITY.
FT	DISULFID	911	923	BY SIMILARITY.
FT	DISULFID	918	932	BY SIMILARITY.
FT	DISULFID	934	947	BY SIMILARITY.
FT	DISULFID	953	964	BY SIMILARITY.
FT	DISULFID	959	973	BY SIMILARITY.
FT	DISULFID	976	988	BY SIMILARITY.
FT	DISULFID	994	1005	BY SIMILARITY.
FT	DISULFID	1000	1014	BY SIMILARITY.
FT	DISULFID	1017	1028	BY SIMILARITY.
FT	DISULFID	1034	1045	BY SIMILARITY.
FT	DISULFID	1040	1054	BY SIMILARITY.
FT	DISULFID	1056	1069	BY SIMILARITY.
FT	DISULFID	1075	1086	BY SIMILARITY.
FT	DISULFID	1081	1095	BY SIMILARITY.
FT	DISULFID	1097	1110	BY SIMILARITY.
FT	DISULFID	1116	1127	BY SIMILARITY.
FT	DISULFID	1122	1136	BY SIMILARITY.
FT	DISULFID	1138	1151	BY SIMILARITY.
FT	DISULFID	1157	1169	BY SIMILARITY.
FT	DISULFID	1164	1178	BY SIMILARITY.
FT	DISULFID	1180	1192	BY SIMILARITY.
FT	DISULFID	1198	1210	BY SIMILARITY.
FT	DISULFID	1204	1219	BY SIMILARITY.
FT	DISULFID	1221	1234	BY SIMILARITY.
FT	DISULFID	1240	1252	BY SIMILARITY.
FT	DISULFID	1246	1261	BY SIMILARITY.
FT	DISULFID	1263	1276	BY SIMILARITY.
FT	DISULFID	1282	1294	BY SIMILARITY.
FT	DISULFID	1289	1303	BY SIMILARITY.
FT	DISULFID	1305	1319	BY SIMILARITY.
FT	DISULFID	1419	1432	BY SIMILARITY.
FT	DISULFID	1427	1441	BY SIMILARITY.
FT	DISULFID	1443	1456	BY SIMILARITY.
FT	DISULFID	1462	1473	BY SIMILARITY.
FT	DISULFID	1468	1482	BY SIMILARITY.
FT	DISULFID	1484	1497	BY SIMILARITY.

FT	DISULFID	1616	1627	BY SIMILARITY.
FT	DISULFID	1622	1636	BY SIMILARITY.
FT	DISULFID	1638	1651	BY SIMILARITY.
FT	DISULFID	1657	1672	BY SIMILARITY.
FT	DISULFID	1667	1681	BY SIMILARITY.
FT	DISULFID	1683	1696	BY SIMILARITY.
FT	CARBOHYD	339	339	POTENTIAL.
FT	CARBOHYD	370	370	POTENTIAL.
FT	CARBOHYD	416	416	POTENTIAL.
FT	CARBOHYD	612	612	POTENTIAL.
FT	CARBOHYD	1042	1042	POTENTIAL.
FT	CARBOHYD	1242	1242	POTENTIAL.
FT	CARBOHYD	1357	1357	POTENTIAL.
SO	SEQUENCE	1712 AA;	166598 MW;	7C924DB1 CRC32;

Query Match
Best Local Similarity 34.1%; Score 103; DB 1; Length 1712;
Matches 15; Conservative 12; Mismatches 12; Indels 4; Gaps 4;

ID	NOV MOUSE	STANDARD:	PRT:	354 AA.
AC	064299;			
DT	01-NOV-1997 (REL. 35, CREATED)			
DT	01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)			
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)			
DE	NOV PROTEIN HOMOLOG PRECURSOR (NOVH).			
GN	NOV.			
OS	MUS MUSCULUS (MOUSE).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUETHERIA; RODENTIA.			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-129/SV. AND ICR. TISSUE-BRAIN;			
RA	SNAITH M.R., NARAYANAN D., TAYLOR L.B., CHOI C.P., MARTINERIE C.,			
RA	PERBAL B., SCHOFIELD P.N., BOUTLER C.A.;			
RL	SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANKS.			
RN	(2)			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-C57BL/6;			
RA	MEDLINE; 96204003.			
RA	MARTINERIE C., CHEVALIER G., RAUSCHER F.J. III, PERBAL B.;			
RL	ONCOGENE 12:1479-1492(1996).			
CC	-1- FUNCTION: IMMEDIATE-EARLY PROTEIN LIKELY TO PLAY A ROLE IN CELL			
CC	GROWTH REGULATION (BY SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING			
CC	PROTEIN FAMILY. CEF-10/CTF6/CTF6/ISF-12/NOV PROTEIN SUBFAMILY.			
CC	-1- SIMILARITY: CONTAINS 1 WFC DOMAIN.			
DR	EMBL; X97863; E1181580;			
DR	EMBL; Y09257; E281106;			
DR	EMBL; X96585; E28599;			
DR	MED: MGI:109185; NOV.			
DR	PROSITE; PS00222; IGF-BINDING; 1.			
DR	PROSITE; PS01185; CTCK_1; 1.			
DR	PROSITE; PS01225; CTCK_2; 1.			
DR	PROSITE; PS01208; WFC; 1.			
KW	PROTO-ONCOGENE; GROWTH FACTOR BINDING; SIGNAL.			
FT	SIGNAL	1	21	POTENTIAL.
FT	CHAIN	22	354	NOV PROTEIN HOMOLOG.
FT	DOMAIN	102	168	WFC.
FT	DOMAIN	261	335	CTCK.
FT	DISULFID	261	298	BY SIMILARITY.
FT	DISULFID	278	312	BY SIMILARITY.
FT	DISULFID	289	328	BY SIMILARITY.
FT	DISULFID	292	330	BY SIMILARITY.
FT	DISULFID	297	334	BY SIMILARITY.
FT	CARBOHYD	91	91	POTENTIAL.
FT	CARBOHYD	277	277	POTENTIAL.

CC soluble variants and fusion proteins with a toxin, imageable
CC compound or radionuclide. Ret3, optionally when expressed from
CC vectors *in vivo*, is used to promote growth of new tissue and
CC survival of damaged tissue, particularly kidney or neural tissue.
CC Typical applications are in renal failure, nephritis, kidney
CC transplants, toxic or hypoxic injury, neurodegeneration, motor
CC neurone disease, multiple sclerosis, bacterial, viral or prion
CC infections (e.g. meningitis, myelopathy associated with HIV or
CC Creutzfeldt-Jakob disease), cranial nerve or spinal cord injury,
CC developmental disorders such as Down's syndrome and cerebral palsy,
CC or conditions involving the peripheral nervous system (Lyme disease,
CC muscular dystrophy and myasthenia gravis). Fusion proteins are
CC used to deliver toxins etc. to Ret-expressing cells, especially
CC tumours.
CC Sequence 1889 BP, 410 A, 569 C, 473 G, 437 T;
50

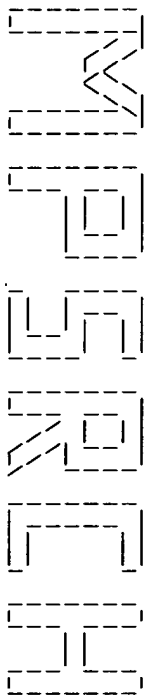
SQ Sequence 1889 BP; 410 A; 569 C; 473 G; 437 T;

Query Match	Score	DB	Length
65.9%	1120	39	1889

Matches 1238; Conservative 0; Mismatches 106; Indels 2; Gaps 1

[illegible]

Oy	807	TCTTCGAGGTTCGGCGTGGGACCCCTCTGTGCAGATCAAGCCTGATGACTTTCTAAAC
Dd	841	ccacgtcaccctactatgagacattcccttgggaacttgtagaacatgagagtcacagatgcctgaga
Oy	867	CCAATGCCACCCTATGGAATCATCTCTGGGACATTGTGCAACTAGACAGTCACGATGTCTAATCA
Dd	901	ggcatctactggggtctgatctggagacgtgccatacccccaaaactcatacgcaagtctcaaat
Oy	927	GGCATTACCTGGGGCTTAATTGGGACGTGCATATCACCCCAAACCTTATCATGCMAGGTCAATAC
Dd	961	tactgttcaccttaagtctcacctgtccaggagcagcgacaacctacagagcagttgtuaan
Oy	987	TACGTTCCTTGCTTAGCTGTACTGTGCCGAGGCAATGTGGCAACCTGAGACAGACATGTGTACAA
Dd	1021	gcttgaaaaggtctctctctccagaaccccctgcctcgttggagagccattgcagctaagatgc
Oy	1047	GCTGAAAATAATCTCTTCTCCAGAACCCCTGCCTCATGTGAGGCCATTGCGGCTAAATATCT
Dd	1081	tttcccaagacagactctttctcccaagagatgggcagactctactcttttcasgtgtgaguc
Oy	1107	TTTTCCACAGACAACCTTTCTCCAGAGACTGGGCGGACCTTAATTTTCTGTGATGCAACA
Dd	1141	gcgaacacagaaacccctgcctcgtatgagactgcagcccgagagctaccactctctctcccat
Oy	1167	GCAACACAGACGCCCTCTGCTTAGGCCCCCACTCAGGCTACGCCCTTGTGCTTTCTTCAAT
Dd	1201	ccttccttgatcttgctgctcagaccctcttggtaagcttggcttctctccagaggtcccttgacc
Oy	1227	CCTTACTGTATTTCTGCTGTGACAGCCCTCTGGTAAGTGGGCTCCCTCTCAGGGTCTCTTGTGTC
Dd	1261	tctccaccacaccagactgatcttcagcctcgttgtgtggagagaacatcgccagcctctgtg
Oy	1287	TCTTCACACACACCACCAACCGACTTGTGATGGAGAGAAAAATGCTGGCCTCTGG
Dd	1321	aagaaagcgcagcgtgtctacacagaa
Oy	1347	AAGAAGATGCACACAGGCTCTACTGCA
RESULT	3	
ID	V00251	standard; cDNA: 1699 BP.
AC	V00251;	
DT	21-MAY-1998	(first entry)
DE	Human Ret ligand; retL3 cDNA.	
KW	Ret ligand; RetL; RetL3; receptor; signal transduction; human;	
KW	cell growth; renal cell; nerve cell; renal failure; nephritis;	
KW	kidney transplant; toxic injury; hypoxic injury;	
KW	neurodegeneration; motor neuron disease; multiple sclerosis;	
KW	Infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;	
KW	cranial nerve injury; spinal cord injury; Down's syndrome;	
KW	cerebral palsy; Lyme disease; muscular dystrophy;	
OS	Homo sapiens.	
FH	Key	Location/Qualifiers
FT	CDS	175..1377
FT		/*tag= a
PD	MO9744356-AA2.	
DR	27-NOV-1997.	
PT	07-MAY-1997; U07726.	
PR	10-APR-1997; US-017427.	
PR	08-MAY-1996; US-017427.	
PR	07-JUN-1996; US-019300.	
PA	16-JUL-1996; US-021859.	
PA	(BIOJ) BIOGEN INC.	
P1	Cate RL, Hession C, Sanicola-Nadel M:	
DR	WPL: 98-018431/02.	
PT	p-PBSD: W37463.	
PT	New nucleic acid encoding ret receptor ligands and related proteins	
PT	- vectors, transformed cells and antibodies, used for promoting cellular	
PT	growth and improving survival of injured cells, especially renal or	
PT	nerve cells	
PS	Claim 1; Page 82-84; 113pp: English.	



(TM)

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MPsrch_PP protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Mar 8 14:37:58 1999; MasPar time 14.37 Seconds

Tabular output not generated. 447.095 Million cell updates/sec

Title: >US-08-866-354-42
Description: (1-397) from US08866354.pep
Perfect Score: 2962
Sequence: 1 MGLSRSPRPPLVILLVLS.....LRPVLSFILLITLITLW 397

Scoring table:
PAM 150
Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 08
Listing first 45 summaries

Database:

a-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Statistics: Mean 34.465; Variance 144.588; scale 0.238

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	2781	93.9	397	28	M37461 Mouse Ret ligand RetL	4.98e-267
2	2386	79.9	400	28	M37463 Human Ret ligand RetL	1.42e-224
3	2347	79.2	346	28	M37465 Mouse Ret ligand RetL	1.24e-222
4	1977	66.7	315	28	M37462 Human Ret ligand RetL	7.26e-185
5	759	25.6	464	28	M37460 Human Ret ligand RetL	9.15e-62
6	744	25.1	460	28	M37459 Human Ret ligand RetL	2.83e-60
7	708	23.9	465	28	M35333 Human Ret ligand RetL	1.06e-56
8	695	23.5	468	28	M37457 Rat Ret ligand RetL	2.05e-55
9	685	23.5	468	27	M27327 Rat glial cell derive	2.05e-55
10	655	23.5	468	28	M35334 Rat glial cell line-d	2.05e-55
11	566	18.4	346	28	M37458 Human Ret ligand RetL	9.69e-41
12	102	3.4	459	2	R08329 Human Ret ligand RetL	6.48e+00
13	97	3.3	904	1	R05619 Human Ret ligand RetL	1.51e+01
14	91	3.1	144	20	M03523 BIV env and rev exon	4.10e+01
15	93	3.1	146	18	R99489 Genetic ob protein	2.95e+01
16	93	3.1	148	18	R99496 Genetic Met-X-ob prot	2.95e+01
17	91	3.1	308	21	M10667 Human TGF-beta-like c	4.10e+01
18	91	3.1	308	21	M10672 Human TGF-beta-like c	4.10e+01

ID	Score	Query Match	Length	DB ID	Description	Pred. No.
19	91	3.1	308	21	M10668 Human TGF-beta-like c	4.10e+01
20	91	3.1	308	21	M10671 Human TGF-beta-like c	4.10e+01
21	91	3.1	308	21	M10666 Human TGF-beta-like c	4.10e+01
22	91	3.1	308	21	M10673 Human TGF-beta-like c	4.10e+01
23	93	3.1	367	26	M29878 Lysophosphatidic acid	2.95e+01
24	92	3.1	1810	16	R34563 Chicken cytolactin	3.48e+01
25	91	3.1	2351	3	P60741 Sequence of human fac	4.10e+01
26	90	3.0	64	16	R86894 Prepro-LAP #2	4.82e+01
27	90	3.0	65	16	R86895 Ob protein fragment #	6.67e+01
28	88	3.0	100	18	M00075 C-terminally truncate	6.67e+01
29	88	3.0	100	18	M00065 C-terminally truncate	6.67e+01
30	88	3.0	119	18	M00067 C-terminally truncate	6.67e+01
31	88	3.0	128	18	M00069 Generic ob protein	6.67e+01
32	88	3.0	128	20	M01404 Generic ob protein	6.67e+01
33	88	3.0	141	18	M00105 N-terminally truncate	6.67e+01
34	88	3.0	141	18	M00050 Generic ob protein	6.67e+01
35	88	3.0	146	18	R39497 Generic ob protein	6.67e+01
36	88	3.0	146	18	R39498 Human embryonal lung	6.67e+01
37	90	3.0	308	16	R84710 Human TGF-beta-like c	4.82e+01
38	90	3.0	308	21	M10669 Human TGF-beta-like c	4.82e+01
39	90	3.0	308	16	R72097 Human TGF-beta-like c	4.82e+01
40	90	3.0	308	21	M10670 Human TGF-beta-like c	4.82e+01
41	90	3.0	308	21	M10662 Human TGF-beta-like c	4.82e+01
42	90	3.0	318	21	M10663 Human TGF-beta-like c	4.82e+01
43	90	3.0	371	15	R75642 Bovine conglutinin	4.82e+01
44	90	3.0	1481	19	M03740 rchd528 gene product	4.82e+01
45	88	3.0	2351	3	P50319 Human antihemophilic	6.67e+01

ALIGNMENTS

RESULT 1
ID M37461 standard; protein; 397 AA.
AC M37461 (first entry)
DE 21-MAR-1998
DT Mouse Ret ligand RetL3.
KW Ret ligand; RetL; RetL3; receptor; signal transduction; mouse;
KW cell growth; renal cell; nerve cell; renal failure; nephritis;
KW kidney transplant; toxic injury; hypoxic injury;
KW neurodegeneration; motor neuron disease; multiple sclerosis;
KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
KW cranial nerve injury; spinal cord injury; Down's syndrome;
KW cerebral palsy; Lyme disease; muscular dystrophy;
KW myasthenia gravis; tumour; therapy.
OS Mus musculus.
PN M09744356-A2.
PD 27-NOV-1997.
PF 07-MAY-1997; U07726.
PR 10-APR-1997; US-017427.
PR 08-MAY-1996; US-017427.
PR 07-JUN-1996; US-019300.
PR 16-JUL-1996; US-021859.
PA (BIOJ) BIOGEN INC.
PI Cate RL, Hession C, Santicola-Nadel M;
DR WPI: 98-018431/02.
DR N-PSDB: V00249.
PT New nucleic acid encoding ret receptor ligands and related prot-
PT - vectors, transformed cells and antibodies, used for promot-
PT growth and improving survival of injured cells, especially renal
PT nerve cells
PS Claim 2: Page 77-78; 113pp: English.
CC This amino acid sequence comprises mouse Ret ligand (RetL) RetL3,
CC deduced from cDNA clones (see V00249) isolated from an EST
CC database and by 5'RACE. Rat and human RetL1, human RetL2 and RetL3
CC sequences (see M37457-60 and M37462-63) are also claimed. RetL is
CC a key component of the Ret signalling pathway that specifically
CC interacts with Ret receptor protein, triggering Ret dimerisation
CC and/or autophosphorylation of the Ret tyrosine kinase domain.
CC Vectors containing RetL3 DNA and prokaryotic or eukaryotic host
CC cells transformed or transfected with these vectors are claimed, as
CC well as a method for production of RetL3, its soluble variants and
CC fusion proteins with a toxin, imageable compound or radionuclide.
CC RetL3, optionally when expressed from vectors in vivo, is used to

CC promote growth of new tissue and survival of damaged tissue,
 CC particularly kidney or neural tissue. Typical applications are in
 CC renal failure, nephritis, kidney transplants, toxic or hypoxic
 CC injury, neurodegeneration, motor neurone disease, multiple sclerosis,
 CC bacterial, viral or prion infections (e.g. meningitis, myelopathy
 CC associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
 CC spinal cord injury, developmental disorders such as Down's syndrome
 CC and cerebral palsy, or conditions involving the peripheral nervous
 CC system (Lyme disease, muscular dystrophy and myasthenia gravis).
 CC Fusion proteins are used to deliver toxins etc. to Ret-expressing
 CC cells, especially tumours.
 SO Sequence 397 AA;

Query Match 93.9%; Score 2781; DB 28; Length 397;
 Best Local Similarity 92.9%; Pred. No. 4.98e-267;

Matches 369; Conservative 16; Mismatches 12; Indels 0; Gaps 0;

DB 1 mglsprpplmlllvislwpjlgsgnslatentfnscgarkkceanpackaayqh 60
 1 MGLSRSPRPPLVILLVLSLWPLGLTGNSTLPTEENRLVNSCTQARKKCEANPACKAAYQH 60
 DB 61 lgsctslsrplleesamadeleaeqjrnslldrcbrhmkhgtcdlywtvtpa 120
 61 LDSCTFPLSPFSGESATSAACLEAAQOLRNSSLIDCRHRRRKHOATCLDIYTWHPV 120
 DB 121 rslgdyelavspyedvtstskpwmkmlsklmkxpsdclclfamclndkcdrlrkayg 180
 121 RSLGDYELDVSPYEDVTSTSKPWMKNLSKLSMKRPSDCLCFAMCLTNDKCDRLRKAYG 180
 DB 121 RSLGDYELDVSPYEDVTSTSKPWMKNLSKLSMKRPSDCLCFAMCLTNDKCDRLRKAYG 180
 121 RSLGDYELDVSPYEDVTSTSKPWMKNLSKLSMKRPSDCLCFAMCLTNDKCDRLRKAYG 180
 DB 181 eacsgitcgrhclaglrstfexkaeahagqlllcpapedagcgerrrntlpscalps 240
 181 EACSGITCGRHCLAGLRSTFEXKAEAHAGQLLPCAPEDAGCGERRNTIAPSCALPS 240
 DB 181 EACSGITCGRHCLAGLRSTFEXKAEAHAGQLLPCAPEDAGCGERRNTIAPSCALPS 240
 181 EACSGITCGRHCLAGLRSTFEXKAEAHAGQLLPCAPEDAGCGERRNTIAPSCALPS 240
 DB 241 vtpncldlrfcrradprrclndfchchpmldlfgcagcagclaylgilgtamttn 300
 241 VTPNCDLRFRCRADPRLRCLNDFCHCHPMLDLFGCAGCAGCLAYLGILGTAMTTPN 300
 DB 241 VAPRCDLRFRCRADPRLRCLNDFCHCHPMLDLFGCAGCAGCLAYLGILGTAMTTPN 300
 241 VAPRCDLRFRCRADPRLRCLNDFCHCHPMLDLFGCAGCAGCLAYLGILGTAMTTPN 300
 DB 301 flskvntlvalgctrcsgnldodeceqlersfsgnplcvalaakmfhrqlfsqdwads 360
 301 FLSKVNITVALGCTRCSGNLDODECEQLERSFSGNPLCVALAAKMFHRQLFSQDWADS 360
 DB 301 FLSKVNITVALGCTRCSGNLDODECEQLERSFSGNPLCVALAAKMFHRQLFSQDWADS 360
 301 FLSKVNITVALGCTRCSGNLDODECEQLERSFSGNPLCVALAAKMFHRQLFSQDWADS 360
 DB 361 tfsvvqgqnsppalrlqprlpvlslfslppllllqclw 397
 361 TFSVVQGQNSPPALRLQPRLPVLSLFFLITLILQTLW 397
 DB 361 TFSVMOQNSPALRPLRPLVLSFFLITLILQTLW 397
 361 TFSVMOQNSPALRPLRPLVLSFFLITLILQTLW 397

RESULT 2

ID W37463 standard; Protein: 400 AA.
 AC W37463;

DT 21-MAY-1998 (first entry)

DE Human Ret ligand RetL3; receptor; signal transduction; human;
 KW Ret ligand; RetL3; RetL3; receptor; signal transduction; human;
 KW cell growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury;
 KW neurodegeneration; motor neurone disease; multiple sclerosis;
 KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
 KW cranial nerve injury; spinal cord injury; Down's syndrome;
 KW cerebral palsy; Lyme disease; muscular dystrophy;
 KW myasthenia gravis; tumour; therapy.
 OS Homo sapiens.
 PN W09744356-42.
 PD 27-NOV-1997.
 PF 07-MAY-1997: U07726.
 PR 10-APR-1997: US-017427.
 PR 08-MAY-1996: US-017427.
 PR 07-JUN-1996: US-019300.
 PR 16-JUL-1996: US-021859.
 PA (BIOI) BIOGEN INC.
 PI Cate RL, Hession C, Sanicola-Nedel M:
 DR WPI: 98-018431/02.
 DR N-PSDB: V00251.
 PT New nucleic acid encoding ret receptor ligands and related proteins
 - vectors, transformed cells and antibodies, used for promoting cell

PT growth and improving survival of injured cells, especially renal or
 PT nerve cells.
 PS Claim 2: Page 85-86; 113pp; English.

CC This amino acid sequence comprises human Ret ligand (RetL) RetL3,
 CC deduced from cDNA clones (see V00251) isolated from a adult heart
 CC and spinal cord libraries. Rat and human RetL, human RetL2 and
 CC mouse RetL3 sequences (see W37457-62) are also claimed. Human
 CC RetL3 is 34.3% identical to human RetL, 34.9% identical to human
 CC RetL2 and 76.8% identical to murine RetL. Ret ligand is a key
 CC component of the Ret signalling pathway that specifically
 CC interacts with Ret receptor protein, triggering Ret dimerisation
 CC and/or autophosphorylation of the Ret tyrosine kinase domain.
 CC Vectors containing retL3 DNA and prokaryotic or eukaryotic host
 CC cells transformed or transfected with these vectors are claimed, as
 CC well as a method for production of RetL3. Its soluble variants and
 CC fusion proteins with a toxin, imageable compound or radionuclide.
 CC RetL3, optionally when expressed from vectors in vivo, is used to
 CC promote growth of new tissue and survival of damaged tissue,
 CC particularly kidney or neural tissue. Typical applications are in
 CC renal failure, nephritis, kidney transplants, toxic or hypoxic
 CC injury, neurodegeneration, motor neurone disease, multiple sclerosis,
 CC bacterial, viral or prion infections (e.g. meningitis, myelopathy
 CC associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
 CC spinal cord injury, developmental disorders such as Down's syndrome
 CC and cerebral palsy, or conditions involving the peripheral nervous
 CC system (Lyme disease, muscular dystrophy and myasthenia gravis).
 CC Fusion proteins are used to deliver toxins etc. to Ret-expressing
 CC cells, especially tumours.
 SO Sequence 400 AA;

Query Match 79.9%; Score 2366; DB 28; Length 400;
 Best Local Similarity 77.5%; Pred. No. 1.42e-224;

Matches 306; Conservative 52; Mismatches 34; Indels 3; Gaps 3;

DB 6 nprlpvwmlllppslpaaagdprrlscrlmnsclgarkkcgadpcsaayhld 65
 6 NPRLPVWMLLPPSLPAAAGDPRLSCRLMNSCLGARKKCGADPCSAAYHLD 65
 DB 6 SPRP-PLVI-LILVLSLW-LELGTGNSLPTENRLVNSCTQARKKCEANPACKAAYQHD 62
 6 SPRP-PLVI-LILVLSLW-LELGTGNSLPTENRLVNSCTQARKKCEANPACKAAYQHD 62
 DB 66 scstslslpseepvpddcleaaqqlnslslgcmchrrmkhgtcdlywtvtpa 125
 66 SCSTSLSLPSEEPVPDDCLEAAQQLNSLSLIGCMCHRRMKHGTCDLYWTVTPA 125
 DB 63 SCTPSLSPFSGESATSAACLEAAQOLRNSSLIDCRHRRRKHOATCLDIYTWHPV 120
 63 SCTPSLSPFSGESATSAACLEAAQOLRNSSLIDCRHRRRKHOATCLDIYTWHPV 120
 DB 126 lgnvelavspyedvtstskpwmkmlsklmkxpsdclclfamclndkcdrlrkayg 180
 126 LGNVELAVSPYEDVTSTSKPWMKNLSKLSMKRPSDCLCFAMCLTNDKCDRLRKAYG 180
 DB 123 LGDYELDVSPYEDVTSTSKPWMKNLSKLSMKRPSDCLCFAMCLTNDKCDRLRKAYG 180
 123 LGDYELDVSPYEDVTSTSKPWMKNLSKLSMKRPSDCLCFAMCLTNDKCDRLRKAYG 180
 DB 186 csqphqgrhclaglrstfexkaeahagqlllcpapedagcgerrrntlpscalps 240
 186 CSQPHQGRHCLAGLRSTFEXKAEAHAGQLLPCAPEDAGCGERRNTIAPSCALPS 240
 DB 183 CSQPHQGRHCLAGLRSTFEXKAEAHAGQLLPCAPEDAGCGERRNTIAPSCALPS 240
 183 CSQPHQGRHCLAGLRSTFEXKAEAHAGQLLPCAPEDAGCGERRNTIAPSCALPS 240
 DB 246 pncldlrfcrradprrclndfchchpmldlfgcagcagclaylgilgtamttn 300
 246 PNCDLRFRCRADPRLRCLNDFCHCHPMLDLFGCAGCAGCLAYLGILGTAMTTPN 300
 DB 243 PNCDLRFRCRADPRLRCLNDFCHCHPMLDLFGCAGCAGCLAYLGILGTAMTTPN 300
 243 PNCDLRFRCRADPRLRCLNDFCHCHPMLDLFGCAGCAGCLAYLGILGTAMTTPN 300
 DB 306 svntsvaalscrrsgnldodeceqlersfsgnplcvalaakmfhrqlfsqdwads 360
 306 SVNTSVAAALSCRRSGNLDODECEQLERSFSGNPLCVALAAKMFHRQLFSQDWADS 360
 DB 303 SKVNITVALGCTRCSGNLDODECEQLERSFSGNPLCVALAAKMFHRQLFSQDWADS 360
 303 SKVNITVALGCTRCSGNLDODECEQLERSFSGNPLCVALAAKMFHRQLFSQDWADS 360
 DB 366 avmahqnpavrrpqpwpalslscclppllllqclw 400
 366 AVMAHQNPVRRPQPWPALSLSCCLPPLLLLQCLW 400
 DB 363 SVMQOQNSPALRPLRPLVLSFFLITLILQTLW 397
 363 SVMQOQNSPALRPLRPLVLSFFLITLILQTLW 397

RESULT 3

ID W37465 standard; Protein: 346 AA.
 AC W37465;

DT 21-MAY-1998 (first entry)

DE Mouse Ret ligand RetL3 partial sequence.
 KW Ret ligand; RetL3; RetL3; receptor; signal transduction; mouse;
 KW cell growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury;
 KW neurodegeneration; motor neurone disease; multiple sclerosis;
 KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;

	KW	cerebral nerve injury; spinal cord injury; Down's syndrome;
	KV	cerebral palsy; Lyme disease; muscular dystrophy;
	KM	myasthenia gravis; tumour; therapy.
	OS	Mus musculus.
	PN	W09744356-A2.
	PD	27-NOV-1997.
	PE	07-MAY-1997: U07726.
	PF	10-APR-1997: US-017427.
	PR	08-MAY-1996: US-017427.
	PR	07-JUN-1996: US-019300.
	PR	16-JUL-1996: US-021859.
	PA	(BioJ) BIOGEN INC.
	PI	Cate RL, Heaston C, Sanicola-Nadel M;
	DR	WPI: 98-018431/02.
	N-PSDS:	V00236.
	PT	New nucleic acid encoding ret receptor ligands and related proteins
	PT	- vectors, transformed cells and antibodies, used for promoting cell
	PT	growth and improving survival of injured cells, especially renal or
	PT	nerve cells
	PS	Disclosure: Page 73-74: 11pp: English.
	CC	This polypeptide comprises a partial sequence of mouse Ret ligand
	CC	RetL3, deduced from EST A4050083 cDNA (see V00255). A full-length
	CC	mouse RetL3 sequence (see W37461) was also obtained. Rat, mouse
	CC	and human RetL1, RetL2 and RetL3 cDNA sequences (see V00245-51) and
	CC	encoded polypeptides (see W37457-63) are claimed and can be used
	CC	in methods for promoting cell growth and improving survival of
	CC	cells, especially renal or neural cells.
	SQ	Sequence 346 AA;
	Query March	79.2% Score 2347; DB 28; Length 346;
	Best Local Similarity 93.9%; Pred. No. 1.24e-222;	
	Matches 310; Conservative 10; Mismatches 10; Indels 0; Gaps 0;	
Db	17	LSPDLPleesamsadcleaaeqirnsjldcrchrnkhqatcldiywvnparslgdy 76
OY	68	LSSPLPSESMTSAACLEAAOQLNSSLIDRCRRKKNHQTCLDIWTYVHPVNSLDYE 127
Db	77	Ldvsydedvtskwpkmnlslklnmlkpdsdlcllfamcltldhkcdtlrkaygeacsglr 136
OY	128	LdvspyedvtvtskmpkwnlslkslmklpdsdcltfamlctlnDCDLRLRKAYGACSGIR 187
Db	137	cqrhlclagqlrsffekaeshagnqlljpcrpedagcgerrrrntlapascpstpnpcld 196
OY	188	CQRHLCLAQQLRSFFEKAEASHAGQLLCPCAPEDAGCGERRRRNTIAPSCALPVAAPCLD 247
Db	197	lsrfceddpilgrsrilmfdgqhchpmndlygtcategsrclraylgllgtamtprnfiskvt 256
OY	248	LRSTCRADPLCRSRIMDMOTCHPHMDILGTATEDSRLRAYLGLIGTAMTPNFISKVNT 307
Db	257	tvaistcrtsgsnlqdeceqlerqsfsgqpncivleaakmrfrhgllfsqdwdastfsvvg 316
OY	308	TVALGCCTRGSGNLQDECEQLERQSFPNQPCLMEMIAAKMRFRHQLFSDQWADRSTFSVMQQ 367
Db	317	gnspnapitlpripilisfstipilligtclw 346
OY	368	GNSPPALRPOLRLPYLSFFILLTLRIQLTW 397
RESULT	4	
ID	W37462 standard; Protein: 315 AA.	
AC	W37462;	
DT	21-MAY-1998 (first entry)	
DE	Human Ret ligand RetL3 partial sequence.	
KW	Ret ligand; RetL; RetL3; receptor; signal transduction; human;	
KM	cell growth; renal cell; nerve cell; renal failure; nephritis;	
KM	kidney transplant; toxic injury; hypoxic injury;	
KM	neurodegeneration; motor neuron disease; multiple sclerosis;	
KW	infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;	
KW	cerebral nerve injury; spinal cord injury; Down's syndrome;	
KW	cerebral palsy; Lyme disease; muscular dystrophy;	
KM	myasthenia gravis; tumour; therapy.	
OS	Homo sapiens.	
PN	W09744356-A2.	

	PE	27-NOV-1997.	
	PF	07-MAY-1997.	U00726.
	PR	10-APR-1987:	US-017427.
	PR	08-MAY-1996:	US-017427.
	PR	07-JUN-1996:	US-019300.
	PR	16-JUL-1996:	US-021859.
	PA	(BIOJ) BIOGEN INC.	
	PI	Cate RL, Heesion C, Sanicola-Nadel M;	
	DR	WPI: 98-018431/02.	
	N-PSDB:	V00250.	
	PT	New nucleic acid encoding ret receptor ligands and related proteins	
	PT	- vectors, transformed cells and antibodies, used for promoting cell	
	PT	growth and improving survival of injured cells, especially renal co-	
	PT	nave cells	
	PS	Claim 2: Page 81-82: 113pp; English.	
	CC	This amino acid sequence comprises a human Ret ligand (RetL) RetL3	
	CC	partial polypeptide sequence, deduced from a partial clone (see	
	CC	V00250) isolated from a human adult heart cDNA library: a	
	CC	full-length RetL3 sequence (see W37463) is also claimed, as well	
	CC	as rat and human RetL1, human RetL2 and mouse RetL3 sequences	
	CC	(see W37455-61). Ret Ligand is a key component of the Ret	
	CC	signalling pathway that specifically interacts with Ret receptor	
	CC	protein, triggering Ret dimerisation and/or autophosphorylation of	
	CC	the Ret tyrosine kinase domain. Vectors containing RetL3 DNA and	
	CC	prokaryotic or eukaryotic host cells transformed or transfected	
	CC	with these vectors are claimed, as well as a method for production	
	CC	of RetL3, its soluble variants and fusion proteins with a toxin,	
	CC	imageable compound or radionuclide. RetL3, optionally when	
	CC	expressed from vectors in vivo, is used to promote growth of new	
	CC	tissue and survival of damaged tissue, particularly kidney or	
	CC	neural tissue. Typical applications are in renal failure,	
	CC	nephritis, kidney transplants, toxic or hypoxic injury,	
	CC	neurodegeneration, motor neurone disease, multiple sclerosis,	
	CC	bacterial, viral or prion infections (e.g. meningitis, myelopathy	
	CC	associated with HIV or Creutzfeldt-jakob disease), cranial nerve or	
	CC	spinal cord injury, developmental disorders such as Down's syndrome	
	CC	and cerebral palsy, or conditions involving the peripheral nervous	
	CC	system (lyme disease, muscular dystrophy and myasthenia gravis).	
	CC	System proteins are used to deliver toxins etc. to Ret-expressing	
	CC	cells, especially tumours.	
SQ	Sequence	315 AA:	
Db	Query Match	66.7%;	Score 1977; DB 28; Length 315;
	Best Local Similarity	81.0%;	Pred. No. 7.26e-185;
	Matches	252; Conservative	31; Mismatches 28; Indels 0; Gaps 0;
Db	OY	5 tptqjrnssllgcmchrrmqvgaeldiyevrharisignyelddspredvtstpxwml 64	
		: : : : : : : : : : : :	
		: : : : : : : : : : : :	
OY	87 AQQIRNSSLLDRCRRHRRKKHOATCLLDLYVVHVHPVRISGDVELDVSPEDVTSTPKMKNL 146		
Db	65 sklmilxpdadclikfamlctclndkedrlfkaygeacsgphcgrhvltirgljffefkaae 124		
	: :		
OY	147 SKLSMKRPDSOLCKAFMLCITLNKDCRLRKRAIGEACSGIRCORHLCLADLRSEFFAAE 206		
Db	125 phagqlllpcapardrcgcerrtnlapncalppvapnclelrilcfdsblcrslvdfq 184		
	: :		
OY	207 SHAOGLLILCPAPEDACGGERRRWTIAPSCALPFAVPNCIDLRNFCRADPLCRSLMDFO 266		
Db	185 thcpmndlgccatcgscrclraylgilgtamtprfvsnrvntsvalectcrgsgnlgceee 244		
	: :		
OY	267 THCHPMILIGCATGEORNCRLRAYLGILGTAMTPNFISKVNTIVVALGCTCGSGNLDOECE 326		
Db	245 mlegffshnpcltaeaakamfhbaqlfsqdwphbtfvmaqhnenpenrvpqwpafsc 304		
	: :		
OY	327 QLESFSONPCFLMAIYIAAKKRHFHQLTSODMASTFSVMQOONSSPALRFQRLRPVSFF 386		
Db	305 tlpiilllislw 315		
	: :		
OY	387 ILTLILLQTWN 397		
RESULT	5		
ID	W37460 standard; Protein; 466 AA.		

AC W37460-1998 (first entry)
21-MAY-1998
Human Ret. Ligand RetL2.
KW Ret. Ligand; RetL; receptor; signal transduction; human;
KW cell growth; renal cell; nerve cell; renal failure; nephritis;
KW kidney transplant; toxic injury; hypoxic injury;
KW neurodegeneration; motor neurone disease; multiple sclerosis;
KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
KW cranial nerve injury; spinal cord injury; Down's syndrome;
KW cerebral palsy; Lyme disease; muscular dystrophy;
KW myasthenia gravis; tumour; therapy.
OS Homo sapiens.
PN M09744356-AZ.
PD 27-NOV-1997.
PF 07-MAY-1997; U07726.
PR 10-APR-1997; US-017427.
PR 08-MAY-1996; US-017427.
PR 07-JUN-1996; US-019300.
PR 16-JUL-1996; US-021859.
PA (BIO) BIOGEN INC.
PI Cate RL, Hession C, Santicola-Nadel M;
DR WPI: 98-018431/02.
DR N-PSDB: V00248.
PT New nucleic acid encoding ret receptor ligands and related proteins
PT - vectors, transformed cells and antibodies, used for promoting cell
PT growth and improving survival of injured cells, especially renal or
PT nerve cells
PS Claim 2: Page 69-70; 113pp: English.
CC This amino acid sequence comprises human Ret Ligand (RetL) RetL2,
CC deduced from a cDNA clone (see V00248) isolated from a human foetal
CC liver library. Rat and human RetL1 and human and mouse RetL3
CC sequences (see W37457-59 and W37461-63) are also claimed. Human
CC RetL2 is 49.1% identical to human RetL1 protein. RetL is a
CC key component of the Ret signalling pathway that specifically
CC interacts with Ret receptor protein, triggering Ret dimerisation
CC and/or autophosphorylation of the Ret tyrosine kinase domain.
CC Vectors containing retL2 DNA and prokaryotic or eukaryotic host
CC cells transformed or transfected with these vectors are claimed, as
CC well as a method for production of RetL2, its soluble variants and
CC fusion proteins with a toxin, imageable compound or radionuclide.
CC RetL2, optionally when expressed from vectors in vivo, is used to
CC promote growth of new tissue and survival of damaged tissue,
CC particularly kidney or neural tissue. Typical applications are in
CC renal failure, nephritis, kidney transplants, toxic or hypoxic
CC injury, neurodegeneration, motor neurone disease, multiple sclerosis,
CC bacterial, viral or prion infections (e.g. meningitis, myelopathy
CC associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
CC spinal cord injury, developmental disorders such as Down's syndrome
CC and cerebral palsy, or conditions involving the peripheral nervous
CC system (Lyme disease, muscular dystrophy and myasthenia gravis).
CC Fusion proteins are used to deliver toxins etc. to Ret-expressing
CC cells, especially tumours.
QO Sequence 464 AA;

	Query Match	25.6%	Score 759;	DB 282;	Length 464;
	Best Local Similarity	37.3%	Pred. No. 9,156	62;	
	Matches 120;	Conservative	78;	Mismatches 99;	Indels 25; Gaps 18;
Dd	40	cvranelcaaesncsyyrflrgc--lagr-dntlankeoaalevlgseplydcrc	95		
Oy	41	CTQARRKCEANPCAKAYOHLDSTPLSPSPSGESATGACILEAQQLRNSLDCRC	100		
Dd	96	krmgkkelgclgylwshlgltege-eftyaspeyprtslglfflaafstgtdprrv	154		
Oy	101	HRKKHATGLDIDITWYHNPRLSDIEL-DVSEFEDVLT--SKPMKK-NL-S-K-L-SML	152		
Dd	155	saksnhcldaekacnldncklrrssylsiscnfeisptercsnrrkchkalqgfdrvpse	214		
Oy	153	KPDSDLCKRAMCTLMDCKRLKKAAGEKCS-GI----RCQRLCLDAQLRSPFEKAAS	207		
Dd	215	ylyrmfscs-gqga-caeritgllpsscyekekncpndilgyvrtthlctsriladth	272		
Oy	208	HAGGLLCPAPADGACGERRMTIAPSLPSVA-PNCLDLSFCRADPLCLSRIMDDQ	266		

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Db 273 accrsayvtvscsdnyagaglyaeimfgdmtprnyvdsppcscrgcsmme 332
QY 267 THCHPM-DILGKATGEGR-CLRAYLGIGIAGMAPNPNISKVNTTVALG--CTCRGSSNLQ 322
Db 333 geecelfirdtcenpqlmaiaqa 354
QY 323 DECEQLKSFSONPCLMEATAIA 344

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AC AC W37459; 21-MAY-1998 (first entry)
 DE Human Ret ligand RetL1.
 KW Ret ligand; RetL; receptor; signal transduction; human;
 KW cell growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury;
 KW neurodegeneration; motor neuron disease; multiple sclerosis;
 KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
 KW cranial nerve injury; spinal cord injury; Down's syndrome;
 KW cerebral palsy; Lyme disease; muscular dystrophy;
 KW myasthenia gravis; tumour; therapy.
 OS Homo sapiens.
 PN M09744356-A2.
 PD 27-NOV-1997.
 PF 07-MAY-1997; 007726.
 PR 10-APR-1997; US-017427.
 PR 08-MAY-1996; US-017427.
 PR 07-JUN-1996; US-019300.
 PR 16-JUL-1996; US-021859.
 PA (BL07) BIOGEN INC.
 PI Cate RL, Hession C, Sanicola-Nadel M;
 DR WPI; 98-018431/02.
 DR N-PSDB; V00247.
 PT New nucleic acid encoding ret receptor ligands and related proteins
 PT - vectors, transformed cells and antibodies, used for promoting cell
 PT growth and improving survival of injured cells, especially renal or
 PT nerve cells
 PS Claim 2; Page 64-66; 113pp; English.
 CC This amino acid sequence comprises human Ret ligand (RetL) RetL,
 CC deduced from cDNA clones (see V00247) isolated from a human
 CC foetal kidney. Rat RetL and mouse and human RetL2 and RetL3
 CC sequences (see W37457 and W37460-63) are also claimed. The
 CC human RetL sequence is 93.3% identical to that of rat. Ret ligand
 CC is a key component of the Ret signalling pathway that specifically
 CC interacts with Ret receptor, triggering Ret dimerisation and/or
 CC autophosphorylation of the Ret tyrosine kinase domain. Vectors
 CC containing retL DNA and prokaryotic or eukaryotic host cells
 CC transformed or transfected with these vectors are claimed, as well
 CC as a method for production of RetL. Its soluble variants and fusion
 CC proteins with a toxin, imageable compound or radionuclide. RetL,
 CC optionally when expressed from vectors in vivo, is used to promote
 CC growth of new tissue and survival of damaged tissue, particularly
 CC kidney or neural tissue. Typical applications are in renal failure,
 CC nephritis, kidney transplants, toxic or hypoxic injury,
 CC neurodegeneration, motor neuron disease, multiple sclerosis,
 CC bacterial, viral or prion infections (e.g. meningitis, myelopathy
 CC associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
 CC spinal cord injury, developmental disorders such as Down's syndrome
 CC and cerebral palsy, or conditions involving the peripheral nervous
 CC system (Lyme disease, muscular dystrophy and myasthenia gravis).
 CC Fusion proteins are used to deliver toxins etc. to Ret-expressing
 CC cells, especially tumours.
 CC Sequence 460 AA:

```

Query Match: 35.1% Score 744: DB 28: Length 460:
Best Local Similarity 37.0% Pred. No. 2.83e-60,
Matches 126: Conservative 70; Mismatches 126; Indels 22; Gaps 19.

Db 3 latyfaajl-ldlllseavsggrl-d-cvksaqclkegscktyrlrlgcavgketn 59
- - - - - : : : : : : : : : : : : : : : : : : : : : : : : : :
12 LVLLVLSLWLPDGTGNSLPTENRLVNSTQARKCEANPCKAKAYQHLDSCTSL-SS 70

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Db      241  VTPNCLDRSCRADPLCRSLTLMFOFHCHQMIDLIGCAEAOSSRCRLAYGLIGTMNTPN 300
        |:|::||:|::||:|::||:|::||:|::||:|::||:|::||:|::||:|::||:| 300
Oy      241  VAPNKLDRSCRADPLCRSLRMLPFYHCHPMIDLIGCATEOSSCRLAYGLIGTMNTP 300
Db      301  FISKVNTVALSCCRSGNLQDECEOLERSFSNPCLVAIAAKMFRHFOLFSDOMADS 360
        |||||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:| 360
Oy      301  FISKVNTVALGCTCRGSGNLQDECEOLEKSFSONPCLMEIAIAKNFHHQLFSQDMADS 360
Db      361  TFSVVOQNNSPALRLQRPRLPSFLPILLOTLM 397
        |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:| 397
Oy      361  TFSVVOQNNSPALRLQRPRLPSFLPILLOTLM 397

RESULT      2
ENTRY       A53138 #type complete
TITLE      gas1 homolog - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
          02-Jul-1996
ACCESSIONS AS3138
REFERENCE   A53138
AUTHORS    Del Sal, G.; Collavin, L.; Ruaro, M.E.; Edoml, P.; Saccone, S.; della Valle, G.; Schneider, C.
           Proc. Natl. Acad. Sci. U.S.A. (1994) 91:1848-1852
           Structure, function, and chromosome mapping of the growth-suppressing human homologue of the murine gas1 gene
#cross-references MWUId:q41f3926
#accession   A53138
#status      Preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
##residues  1-345 ##label RES
#cross-references GB:L13699; NID:g472859; PID:g472860
SUMMARY     #length 345 #molecular_weight 35721 #checksum 570

Query Match      3.9%; Score 115; DB 2; Length 345;
Best Local Similarity 31.9%; Pred. No. 2,31e-03;
Matches 22; Conservative 19; Mismatches 24; Indels 4; Gaps 3;

Db      24  LMALQLLGSPKRSGIAGHRRLI--CWQALLQCQGEPECCSYVNYQAEACPVLAQH-G 80
        |::|::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|: 80
Oy      15  LLVLVSIMLPDGSTNSIPTENRYNSCTQARKKCANPACKAAY-OHLDSCTPLSSPLP 73
        :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:| 73
Db      81  GDPAAGAA 89
Oy      74  GGSATSHA 82

RESULT      3
ENTRY       S25771 #type complete
TITLE      gas1 protein - mouse
ORGANISM   #formal_name Mus musculus #common_name house mouse
DATE       13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
          10-Sep-1997
ACCESSIONS S25771
REFERENCE   S25771
AUTHORS    del Sal, G.; Ruaro, M.E.; Phillips, L.; Schneider, C.
           Cell (1992) 70:595-607
           The growth arrest-specific gene, gas1, is involved in growth suppression.
#cross-references MWUId:92370681
#accession   S25771
#status      Preliminary
#molecule_type mRNA
##residues  1-384 ##label DEL
#cross-references EMBL:X65128; NID:g51045; PID:g51046
GENETICS   gas1
KEYWORDS   transmembrane protein
SUMMARY     #length 384 #molecular_weight 40375 #checksum 5181

Query Match      3.9%; Score 115; DB 2; Length 384;
Best Local Similarity 33.9%; Pred. No. 2,31e-03;
Matches 21; Conservative 16; Mismatches 22; Indels 3; Gaps 2;
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Db      58 PALLCJLWALLOLCASRGSLHGRRLI--CQNALCOCGEPPDSCVAASQVAECAPV 115
QY      9 PPPLYVILLVLSLMPLETGNSLPTENRLNVNSTQARKKCEAMPACKAAV--QHLLDSCDPS 67
Db      116 IA 117
QY      68 LS 69

RESULT 4
ENTRY   XYECO2 #type complete
TITLE   adaptive response regulatory protein - Escherichia coli
CONTAINS
ORGANISM
DATE    28-Dec-1987 #sequence_revision 05-Dec-1997 #text_change
ACCESSIONS
REFERENCE
#authors
Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Berna, N.T.;
Burland, V.; Riley, M.; Collado-VIDES, J.; Glasner, J.D.;
Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.;
Kirpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao
Y.
#journal
#title
The complete genome sequence of Escherichia coli K-12.
#cross-references MUID:9742617
#accession
C64991
#status
nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-354 #label BLAT
#cross-references GB:AE000310; GB:U00096; NID:g2367131; PID:g1788542;
UMGP:b2213
#experimental_source strain K-12, substrain MG1655
REFERENCE
#authors
Nakabeppu, Y.; Kondo, H.; Kawabata, S.; Iwanaga, S.;
Sekiyauchi, M.
#journal
J. Biol. Chem. (1985) 260:7281-7288
#title
Purification and structure of the intact Ada regulatory
protein of Escherichia coli K12, O(6)-methylguanine-DNA
methyltransferase.
#cross-references MUID:85207761
#accession
A22630
#molecule_type DNA
#residues 1-133,'R',135-354 #label NAK
#cross-references GB:M10211; NID:g145188; PID:g145189
#experimental_source strain K12
REFERENCE
#authors
Dempfle, B.; Sedgwick, B.; Robins, P.; Totley, N.; Waterfield,
M.D.; Lindahl, T.
#journal
Proc. Natl. Acad. Sci. U.S.A. (1985) 82:2688-2692
#title
Active site and complete sequence of the suicidal
methyltransferase that counters alkylation mutagenesis.
#cross-references MUID:85190562
#accession
A22667
#molecule_type DNA
#residues 1-774,'D',76-78,'PR',81-317,'V',319-329,'S',331-354
#label DEM
#experimental_source strain B/r
REFERENCE
#cross-references GB:M10315; NID:g145190; PID:g145191
#journal
14114
#authors
Nakabeppu, Y.; Sekiyauchi, M.
#journal
Proc. Natl. Acad. Sci. U.S.A. (1986) 83:6297-6301
#title
Regulatory mechanisms for induction of synthesis of
enzymes in response to alkylating agents: Ada protein
as a transcriptional regulator.
#cross-references MUID:86313568
#accession
14114
#status
translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-27 #label RES
#cross-references GB:M13828; NID:g145196; PID:g145197

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OY 121 RSLGDELDVSPYEDVTYSKPMKMLSKMLKPSDCLKFAMLCTLDKCDRLKAYG 180
DB 181 EACSGIRCORHICLAQLRSFEFEKAESHAOGILLCPACAPEDAGCGERRNTIAPSCALPS 240
OY 181 EACSGIRCORHICLAQLRSFEFEKAESHAOGILLCPACAPEDAGCGERRNTIAPSCALPS 240
DB 241 VTPNCLDLRSFCRADPLCLRSRLMDPOTCHPMDIIGTCATEOSRCLRAYLIGLIGTAMTPN 300
OY 241 VTPNCLDLRSFCRADPLCLRSRLMDPOTCHPMDIIGTCATEOSRCLRAYLIGLIGTAMTPN 300
DB 301 FISKVNTTVALSCTCRSGSGLNLODECEOLERSFSQNPCLVEAIAAKMFRHROLFSQDMADS 360
OY 301 FISKVNTTVALSCTCRSGSGLNLODECEOLERSFSQNPCLVEAIAAKMFRHROLFSQDMADS 360
DB 361 TFSVVOOONSPPALRPLQPLPILSFIPLILLOTLM 397
OY 361 TFSVVOOONSPPALRPLQPLPILSFIPLILLOTLM 397

RESULT 2
ID 035325 PRELIMINARY: PRT: 397 AA.
AC 035325:
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DE GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR FAMILY RECEPTOR ALPHA-3.
GN GFRA-3.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCUROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RA TRUMP M., RAYNOSCHER C., IBANEZ C.F.;
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF020305; G2429367; -.
SQ SEQUENCE 397 AA; 44333 MW; F0C0C841 CRC32;

Query Match 93.8%; Score 2778; DB 11; Length 397;
Best Local Similarity 92.7%; Pred. No. 0.00e+00;
Matches 368; Conservative 17; Mismatches 12; Indels 0; Gaps 0;

DB 1 MGLSPPRPPLMILLVLSLMLPLGAGNSLATENRFVNSTQARRKCEANPACAKAYOH 60
OY 1 MGLSPPRPPLVILLVLSLMLPLGAGNSLATENRFVNSTQARRKCEANPACAKAYOH 60
DB 61 LGSCTSSLSRPLPLEESAMADCLAEAEOLRNSSLIDCRHRMKHOATCDIYTVHPA 120
OY 61 LGSCTSSLSRPLPLEESAMADCLAEAEOLRNSSLIDCRHRMKHOATCDIYTVHPA 120
DB 121 RSLGDELDVSPYEDVTYSKPMKMLSKMLKPSDCLKFAMLCTLDKCDRLKAYG 180
OY 121 RSLGDELDVSPYEDVTYSKPMKMLSKMLKPSDCLKFAMLCTLDKCDRLKAYG 180
DB 121 RSLGDELDVSPYEDVTYSKPMKMLSKMLKPSDCLKFAMLCTLDKCDRLKAYG 180
OY 121 RSLGDELDVSPYEDVTYSKPMKMLSKMLKPSDCLKFAMLCTLDKCDRLKAYG 180
DB 181 EACSGIRCORHICLAQLRSFEFEKAESHAOGILLCPACAPEDAGCGERRNTIAPSCALPS 240
OY 181 EACSGIRCORHICLAQLRSFEFEKAESHAOGILLCPACAPEDAGCGERRNTIAPSCALPS 240
DB 241 VTPNCLDLRSFCRADPLCLRSRLMDPOTCHPMDIIGTCATEOSRCLRAYLIGLIGTAMTPN 300
OY 241 VTPNCLDLRSFCRADPLCLRSRLMDPOTCHPMDIIGTCATEOSRCLRAYLIGLIGTAMTPN 300
DB 301 FISKVNTTVALSCTCRSGSGLNLODECEOLERSFSQNPCLVEAIAAKMFRHROLFSQDMADS 360
OY 301 FISKVNTTVALSCTCRSGSGLNLODECEOLERSFSQNPCLVEAIAAKMFRHROLFSQDMADS 360
DB 361 TFSVVOOONSPPALRPLQPLPILSFIPLILLOTLM 397
OY 361 TFSVVOOONSPPALRPLQPLPILSFIPLILLOTLM 397

RESULT 3
ID 055243 PRELIMINARY: PRT: 397 AA.
AC 055243:

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DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR FAMILY RECEPTOR ALPHA-3.
GN GFRA3.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCUROGNATHI; MURIDAE; MURINAE; MUS.
RN [1]
RP SEQUENCE FROM N.A.
RA WIDENFALK J., TOMAC A., LINDOVIST E., HOFFER B., OLSON L.;
RL SUBMITTED (MAR-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RA NAVEILHAN P., BAUDER C., MIKAELS O., SHEN L., WESTPHAL H., ERNFORS P.;
RL PROC. NATL. ACAD. SCI. U.S.A. 0:0-0(1997).
DR EMBL: AF036163; G2674177; -.
SQ SEQUENCE 397 AA; 44302 MW; F77607CF CRC32;

Query Match 93.4%; Score 2766; DB 11; Length 397;
Best Local Similarity 92.4%; Pred. No. 0.00e+00;
Matches 367; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

DB 1 MGLSPPRPPLMILLVLSLMLPLGAGNSLATENRFVNSTQARRKCEANPACAKAYOH 60
OY 1 MGLSPPRPPLVILLVLSLMLPLGAGNSLATENRFVNSTQARRKCEANPACAKAYOH 60
DB 61 LGSCTSSLSRPLPLEESAMADCLAEAEOLRNSSLIDCRHRMKHOATCDIYTVHPA 120
OY 61 LGSCTSSLSRPLPLEESAMADCLAEAEOLRNSSLIDCRHRMKHOATCDIYTVHPA 120
DB 121 RSLGDELDVSPYEDVTYSKPMKMLSKMLKPSDCLKFAMLCTLDKCDRLKAYG 180
OY 121 RSLGDELDVSPYEDVTYSKPMKMLSKMLKPSDCLKFAMLCTLDKCDRLKAYG 180
DB 121 RSLGDELDVSPYEDVTYSKPMKMLSKMLKPSDCLKFAMLCTLDKCDRLKAYG 180
OY 121 RSLGDELDVSPYEDVTYSKPMKMLSKMLKPSDCLKFAMLCTLDKCDRLKAYG 180
DB 181 EACSGIRCORHICLAQLRSFEFEKAESHAOGILLCPACAPEDAGCGERRNTIAPSCALPS 240
OY 181 EACSGIRCORHICLAQLRSFEFEKAESHAOGILLCPACAPEDAGCGERRNTIAPSCALPS 240
DB 241 VTPNCLDLRSFCRADPLCLRSRLMDPOTCHPMDIIGTCATEOSRCLRAYLIGLIGTAMTPN 300
OY 241 VTPNCLDLRSFCRADPLCLRSRLMDPOTCHPMDIIGTCATEOSRCLRAYLIGLIGTAMTPN 300
DB 301 FISKVNTTVALSCTCRSGSGLNLODECEOLERSFSQNPCLVEAIAAKMFRHROLFSQDMADS 360
OY 301 FISKVNTTVALSCTCRSGSGLNLODECEOLERSFSQNPCLVEAIAAKMFRHROLFSQDMADS 360
DB 361 TFSVVOOONSPPALRPLQPLPILSFIPLILLOTLM 397
OY 361 TFSVVOOONSPPALRPLQPLPILSFIPLILLOTLM 397

RESULT 4
ID 060609 PRELIMINARY: PRT: 400 AA.
AC 060609:
DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE GDNF FAMILY RECEPTOR ALPHA 3.
GN GFRA3.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
SCUROGNATHI; HOMINIDAE; HOMO.
RN [1]
RP SEQUENCE FROM N.A.
RA BALOH R.H., GORODINSKY A., GOLDEN J.P., TANSEY M.G., KECK C.L.,
POPESEU N.C., JOHNSON E.M. JR., MILBRADT J.;
RL PROC. NATL. ACAD. SCI. U.S.A. 0:0-0(1998).
DR EMBL: AF051767; G2961632; -.
SQ SEQUENCE 400 AA; 44538 MW; 6DFB5381 CRC32;

Query Match 79.8%; Score 2363; DB 4; Length 400;

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Best Local Similarity 77.2%; Pred. No. 0.00e+00;
Matches 305; Conservative 53; Mismatches 34; Indels 3; Gaps 3;

Db	6	NPRLPVPVLLMLLLPSPRLPAGBPLPHESTLNMSCLOARRKCOADPTCSAAAYHLD	65
Qy	6	SPRP-PRPLYT-LLVLVLSIM-LPDTGNSLPENLVNSCTDARKKCCANPACRAAYHLD	62
Db	66	SCSSISTPLDSEEPSVPADCLAAAOOLRNSSLIGCMCHRRMRNOVCGLDIYTVHARS	1255
Qy	63	SCPSLSLSPPLSGESATSAACLEAAOOLRNSSLIDCRRHMRKHQATCLDIYTVHBPVS	1222
Db	126	LGNEELDVSPFEDYVTSKPKMKMNSKLNMLKPPSDDLCLFPMCLTLDKDCDLRKAYGEA	1855
Qy	123	LGDELVDVSPFEDYVTSKPKMKMNSKLSMLKPPSDDLCLFPMCLTLDKDCDLRKAYGEA	1822
Db	186	CSGPHCOHVCLLRDLITFEFKAAEPHAGLLCCAPRDNDCGERRRNTIAPNCLPVA	2455
Qy	183	CSGIRCOHCLLAQRLSRFEKAAASHAGLLCCAPEDBAGCGERRRNTIAPSCALPSVA	2422
Db	246	PNCLELRRLCFSDPLCGRSLVDVOTHCHPMDILGTGATGEOGRCLRAYLGLGTAMTENV	3055
Qy	243	PNCLELRRLCFSDPLCGRSLVDVOTHCHPMDILGTGATGEOGRCLRAYLGLGTAMTENV	3022
Db	306	SNVNTSVALLSTCTGCGSGNLOECEMLBEFESHNCLELATAAKKRFHSOLFSDQWHPPTF	3655
Qy	303	SKVNTVALLGCTGCGSGNLOECEQLKESFSQNCLELATAAKKRFHROLFSODMADSTF	3622
Db	366	AVMAHONENPAVRPOWPVPSLFCSTPLPILLLSLM	400
Qy	363	SVMOOQNSPRLRPOLRPLVTSFFILITLILQITLM	397

RESULT	5	
ID	015316	
	015316	
		PRELIMINARY;
		PRT;
		464 AA.

DT 01-JAN-1998 (TREMBLREL, 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL, 05, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMBLREL, 07, LAST ANNOTATION UPDATE)
 DE GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR BETA.
 GN GDNFR-BETA.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA: PRIMATES
 CATARRHINI: HOMINIDAE: HOMO.
 CATHARTIDAE: HOMINIDAE: HOMO.

Query Match	25.68;	Score 759;	DB 4;	Length 464;
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	Matches	120;	Conservative	78;	Mismatches	99;	Indels	25;	Gaps	18
Db	40	CVRANELCAASNSCSRRLTROC	--LAGR-DRTMTLANNCCQAALVLOESPLYORC	95						
Oy	41	CTQAKKCEANPACAAOHLDSCPSLSPSPCESATSAACLEAAQOLNNSLIDRC	100							
Db	96	KRGKMKELQCIQIYWSIHGLTEGE-EFEYEASPYEPYVSRLSIDIFRLASIFSGTGADPVV	154							
Oy	101	HRMKHQATCIDIYTVTHPVRSIDGYEL-DVSPEDVYT--SKPMKM-NL-S-K-L-SML	152							
Db	155	SAKSHHCIDAAKACALNNCKKLBSYISISICNRELSPERCNRKRCHALNQFDRVPSE	214							
Oy	153	KPDSDLCCKFMALCTLNNCKCDRLKRAYEBAOS-GI---RQRHLCALQLNRSFEKAAES	207							
Db	215	YTYRLPFCSC--ODQA-CAERRRQTLTPSCSYEDKEKPNCLDRLGVCRTDHCRLSDLFH	272							
Oy	208	HAQGLLCPAIPAEDEGCGERRRNTIAPSCALPSVA-PCNCLDRSCRADPPLCRSLINDFO	266							
Db	273	ANCRASYOTVWSCPADNTQACLGSYAGMIGFDMPTNYVSSPTGIIVSPMCSRGSGNME	332							

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0Y 267 THCHM-DIGTCAEDSR-CLRAYGLIGTAMTPNFISKVNTVALG--CTCRSGNLQ 322

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Db      333 EECEKEFLRDTENPCLRNAIQ 354
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QY     323 DECEOLEKSFQNPCLMEIAA 344

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RESULT	6	PRELIMINARY;	PRT;	464	AA.
ID	015328				
	015328				

DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE RET LIGAND 2.
 GN RETL2.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES
 OC CARNIVORAE; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE: 97322356.
 RA SANICOLA M., HESSON C. A., WORLEY D. S., CARMILLO P., EHRENFELDS C.,
 RA MALUS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,
 RA PEPIRSKY R. B., CADE R. L.;
 RT "clial cell line-derived neurotrophic factor-dependent RET activation
 RT can be mediated by two different cell-surface accessory proteins.";
 RL PROC. NATL.ACAD. SCI. U.S.A. 94:6238-6243(1997).
 Q0 EMBL: U97145; G2262028; -;
 Q0 SEQUENCE 464 AA; 51543 MW; 288A8BD8 CRC32;

Query Match	25.68;	Score 759;	DB 4;	Length 464;
Best Local Similarity	37.38;	Pred. No. 1.23e-158;		

ID	NAME	PRELIMINARY	PRT	464 AA.
035977				
035977				
01-JAN-1998	(TREMBLREL. 05, CREATED)			
01-JAN-1998	(TREMBLREL. 05, LAST SEQUENCE UPDATE)			
01-NOV-1998	(TREMBLREL. 08, LAST ANNOTATION UPDATE)			
GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR-BETA.				
GN	GDNF-BETA OR RETL2.			
OS	RATTUS NORVEGICUS (RAT).			
OC	EUFAROTA, METAOA, CHORDATA, VERTEBRATA, MAMMALIA: EUTHERIA: RODENTIA.			
CC	SCUROGNATHI: MORIDAE: MORINAE; RATTUS.			
GN	[1]			

RESULT	7		
ID	035977	PRELIMINARY;	PRT; 464 AA.
AC	035977;		
DT	01-JAN-1998 (TREMBLREL_05, CREATED)		
DT	01-JAN-1998 (TREMBLREL_05, LAST SEQUENCE UPDATE)		
DT	01-NOV-1998 (TREMBLREL_08, LAST ANNOTATION UPDATE)		
DE	GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR-BETA		
GN	GDNFR-BETA OR RETL.		
OS	RATTUS NORVEGICUS (RAT).		
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHER		
SC	SCUROGNATHI; MURIDAE; MURINAE; RATTUS.		
IN	[1]		

DT 01-JAN-1998 (TREMBAI.REL. 05, LAST SOURCE UPDATE)
 DT 01-NOV-1998 (TREMBAI.REL. 08, LAST ANNOTATION UPDATE)
 DE GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR-BETA
 GS GDNFR-BETA OR RETL2.
 GN RATTUS NORVEGICUS (RAT).
 OC EURABOT: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA
 CC SCUROGNATHI: MURIDAE: MURINAE: RATTUS.
 NN [1]

RP SEQUENCE FROM N.A.
 RA TRUMP M., RAYNOSCHER C., IBANEZ C.F.;
 RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RC SEQUENCE FROM N.A.
 RC TISSUE-BRAIN/KIDNEY;
 RX MEDLINE: 97322356.
 RA SANICOLA M., HESSON C.A., WORLEY D.S., CARMILLO P., EHRENFELDS C.,
 RA WALUS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,
 RA PEPINSKY R.B., CATE R.L.;
 RT "Glial cell line-derived neurotrophic factor-dependent RET activation
 can be mediated by two different cell-surface accessory proteins."
 RL PROC. NATL. ACAD. SCI. U.S.A. 94:6238-6243(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN/KIDNEY;
 RA SANICOLA M., HESSON C.A., WORLEY D.S., CARMILLO P., EHRENFELDS C.,
 RA WALUS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,
 RA PEPINSKY R.B., CATE R.L.;
 RT SUBMITTED (APR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: U97143; G2282024; .
 SO SEQUENCE 464 AA; 51668 MW; B1A2BD11 CRC32;
 Query Match 25.5%; Score 754; DB 11; Length 464;
 Best Local Similarity 37.6%; Pred. No. 2,446-157;
 Matches 121; Conservative 74; Mismatches 102; Indels 25; Gaps 18;
 Db 40 CYRANELCAESNCSSRRTRLQC---LAGR-DRTMTLANKCOALEVLOSPYDRC 95
 Qy 41 CQARKKCEANPACAAVOHLDSCPSLSPSGESATSAACLEAQLRANSLIDRC 100
 Db 96 KGMKKELOCIQVYSHHGLTGE-EPEYASPYEPTVSRSLDIRLASITSGTDPAY 154
 Qy 101 HRMHQATCLDIYTVHVRSLGDEL-DVSPYEDVT--SKPMK-NL-S-K-L-SML 152
 Db 155 STKSHCLDAKACNINCKKLRSSYSISICNREISPTERCNRRCCHALQEPFRVSE 214
 Qy 153 KPDSOLCLKFMCTLNCKCDRLKRAVGECS-GI---KORHICLALQLSFFKAAES 207
 Db 215 YTRKLFQSC-ODQA-CAERRRQTLIPSCSYEDKEKPCLDRLSICRTDHLCSRLADFH 272
 Qy 208 HAOGILCPACAPEDAGCERRRNTIAPSCALPSVA-PNCIDLRSCGRADPLCRSLMDFO 266
 Db 273 ANCRASYTITSCPADNQACLGSAAGIGEDMTNPYVDSNPTGIVVSPWNCROSGNME 332
 Qy 267 THCHPM-DILGICATEOSR-CLRALGLIGTAMTPNFIKSVNTVALG--CTCRGSGNGL 322
 Db 333 ECEKFLRDEFTENPCLRNAIOA 354
 Qy 323 DECEOLEKSFSONPCLMEALIA 344
 RESULT 8
 ID 015507 PRELIMINARY; PRT: 460 AA.
 AC 015507;
 DT 01-JAN-1998 (TREMBREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBREL. 05, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBREL. 08, LAST ANNOTATION UPDATE)
 DE RET LIGAND 1.
 GN RETL.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
 OC CATARRHINI; HOMINIDAE; HOMO.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-KIDNEY;
 RX MEDLINE: 97322356.
 RA SANICOLA M., HESSON C.A., WORLEY D.S., CARMILLO P., EHRENFELDS C.,
 RA WALUS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,
 RA PEPINSKY R.B., CATE R.L.;
 RT "Glial cell line-derived neurotrophic factor-dependent RET activation
 can be mediated by two different cell-surface accessory proteins.";

RL PROC. NATL. ACAD. SCI. U.S.A. 94:6238-6243(1997).
 RN [2]
 RC SEQUENCE FROM N.A.
 RC TISSUE-KIDNEY;
 RA SANICOLA M., HESSON C.A., WORLEY D.S., CARMILLO P., EHRENFELDS C.,
 RA WALUS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,
 RA PEPINSKY R.B., CATE R.L.;
 RT SUBMITTED (APR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-SUBSTANTIA NIGRA;
 RA HISIKI T., KONDOH K., ICHIMITA S., NIMURA Y., SEKI N., OZAKI T.,
 RA SAKIYAMA S., TAKAHASHI H., OHNUMA N., TANABE M., FUJIMURA S.,
 RA NAKAGAWARA A.;
 RT SUBMITTED (OCT-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: U97144; G2282026; .
 DR EMBL: U95847; G2459742; .
 SO SEQUENCE 460 AA; 50838 MW; 022FECA CRC32;
 Query Match 25.1%; Score 744; DB 4; Length 460;
 Best Local Similarity 37.0%; Pred. No. 9,606-155;
 Matches 128; Conservative 70; Mismatches 126; Indels 22; Gaps 19;
 Db 3 LATYFALPL-LDILLSAEVSGDRL-D-CVKASDCLKEQSCSTKYRTLQCVAGRETN 59
 Qy 12 LVILLVLSLWPLGTGNSLPTENRLVNSTQARKKCEANPACAAVOHLDSCPSL-SS 70
 Db 60 FSLASGLEAKDE-CRSAMEALKKSLNCRCKRMKKEKNCRLRYSMY--OSIQGDLL 116
 Qy 71 -PLPSGESATSAACLEAQLRANSLIDRCRHRMKHQATCLDIYVHVRSLGDEL- 128
 Db 117 EDSPYE-PVNSRLSDIFRVYFISVEHPIKGNCLDAKACNLDIDCKKYSAYITPCTT 175
 Qy 129 DVSPYEDVTSKPMK-NLSK-LSMK-PDSOLCLKFMCTLNCKCDRLKRAVGECS- 184
 Db 176 SVSNDVNCRRCHALQEPFRVSEPAKHSYGLFCSC-R-DIATERRQTVPCSYEER 233
 Qy 185 GIR---CORHICLALQLSFFKAAESHAOGLLCPACAPEDAGCERRRNTIAPSCALPSV 241
 Db 234 EKPNCLDQSCNTYICRSRLADFTNCPESRSVSSCLKENYADCLLAYSGLIGIVMT 293
 Qy 242 A-PNCLDLRSCGRADPLCRSLMDFOYCHPMOI-LGTCTED-SRLRLAYLGLIGTAMT 298
 Db 294 PNYSIDSSLSVAPWCDCSNGNDLECLKFLNFKDTCCKNAIOA 339
 Qy 299 PNFIKSVNTVALGCTCRGSGNIDCEOLEKSFSONPCLMEALIA 344
 RESULT 9
 ID 035252 PRELIMINARY; PRT: 463 AA.
 AC 035252;
 DT 01-JAN-1998 (TREMBREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBREL. 05, LAST SEQUENCE UPDATE)
 DT 01-JAN-1998 (TREMBREL. 05, LAST ANNOTATION UPDATE)
 DE GDNF RECEPTOR BETA.
 GN GDNF-BETA.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
 OC SCIUROGNATHI; MURIDAE; MURINAE; MUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57;
 RA DEY B.K., WONG Y.W., TOO H.P.;
 RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AF015172; G2624963; .
 SO SEQUENCE 463 AA; 51134 MW; 910EP17F CRC32;
 Query Match 25.1%; Score 742; DB 11; Length 463;

Query Match	77.2%	Score 1803;	DB 28;	Length 466;
Best Local Similarity	53.3%	Pred. No. 1.33e-159;		
Matches 255;	Conservative	23;	Mismatches 183;	Indels 17; Gaps 12.
1 mflatlyfalplldlmsaevsgdrl--devksdqglbkqsgsttyrtlrqcvagket 58	16 MXLKLSLALPLKXXLLQGAELGXKRLXXDVCVAXXXCXAXKXCSXXYYRTLRQCVAGKXX 75			
59 nfsalstglaekde--craamealbkqslyncrcrgrmkbkcnclrlywsmysiq-gndl 115	76 NTXKLASGEXKXXKXXCXAXEXLXXSSLSYDRCRCRGMKKEXXCLXIYWSXHXKXLLGXGXX 135			
116 ledspyeep-vnsrlsdlfravplfsdvfgqvvehlskgnncldaakcnldtckkyrsay 174	136 LEXSPYEYEVXVTSRLSDIRFXKXXSXXSXXKXXDXKXXKXSKXCIDAKACMLNDXCKRLASAY 195			
175 ltpcrtamsn-evcnrrtrchkalrgfdkvpakhsygmflfscsr--dlaccerrrtitvp 231	196 IXXKXXXXXXKXERCKRRKCHKALRQEFKQVPPKXHYIGLFFSCXKXXDXACKERRRQITXP 255			

Dc 232 vcsyeerpcplslqsgcdkfyrcrcladffncgpearsvsncklkyadcllaesg 291
Db 256 SCSIEHXEKPRCLDLRXKCRDNLCSRRLADFNXCAXXXXXXRYVSCAAMHYXXKLAYVG 315
Qy 292 lfgtwmfpnyvdas-sls-vapwcdcasngndledclklnifidntclkaqlaqfngs 749
Db 316 LIGFXTMPNYVDSSXTXXXVAPMCXCGSGSXGXECEKEFLFXFXNPCLKNALIOAFGN:X 800
Qy 350 dvtmwge-p-ptygttatlttafvknkp-lgspsgene-lpthvlppcalldgyt 851
Db 376 XXXXXXXXXXXXFVVXXXXXXXXXXITAKHXXXXXPSTLXXXXSXXXXXLXTYVXXXXXLOW:NH 900
Qy 404 ksvysgethlclsdgdfgdglagasshttkmsappscalseljpmltalalalls 951
Db 436 KXNXSKEXXCFXELTNTNXXXSOSXXXXXXSXAAFPXALKLPVLMLTLALAXLLS 1000
RESULT 4
ID W37460 standard; Protein: 464 AA.
AC M37460;
DC 21-MAY-1998 (first entry)
DE Human Ret. ligand RetL2.
KW Ret ligand; RetL; RetL2; receptor; signal transduction; human:
KW cell growth; renal cell; nerve cell; renal failure; nephritis;
KW kidney transplant; toxic injury; hypoxic injury;
KW neurodegeneration; motor neurone disease; multiple sclerosis;
KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
KW cranial nerve injury; spinal cord injury; Down's syndrome;
KW cerebral palsy; Lyme disease; muscular dystrophy;
KW myasthenia gravis; tumour; therapy.
OS Homo sapiens.
PN MOJ744356-A2.
PS 27-NOV-1997.
PF 07-MAY-1997; U07726.
PE 10-APR-1997; US-017427.
PR 08-MAY-1996; US-017427.
PR 07-JUN-1996; US-019300.
PR 16-JUL-1996; US-021859.
PA (BIOJ.) BIOGEN INC.
PI Cate RL, Hession C, Santicola Nadel M,
DR WP1: 98-018431/02.
NR N-PDSB: V00248.
PT New nucleic acid encoding ret receptor ligands and related proteins
PT - vectors, transformed cells and antibodies, used for promoting cell
PT growth and improving survival of injured cells, especially renal or
PT nerve cells
P1 Claim 2; Page 69-70; 113pp: English.
P5 This amino acid sequence comprises human Ret ligand (RetL) RetL2,
CC deduced from a cDNA clone (see V00248) isolated from a human foetal
CC liver library. Rat and human RetL1, and human and mouse RetL3
CC sequences (see W37457-59 and W37461-63) are also claimed. Human
CC RetL2 is 49.1% identical to human RetL1 protein. RetL is a
CC key component of the Ret signalling pathway that specifically
CC interacts with Ret receptor protein, triggering Ret dimerization
CC and/or autophosphorylation of the Ret tyrosine kinase domain.
CC Vectors containing retL2 DNA and prokaryotic or eukaryotic host
CC cells transformed or transfected with these vectors are claimed, as
CC well as a method for production of RetL2, its soluble variants and
CC fusion proteins with a toxin, imageable compound or radionuclide.
CC RetL2, optionally when expressed from vectors in vivo, is used to
CC promote growth of new tissue and survival of damaged tissue.
CC Particularly kidney or neural tissue. Typical applications are in
CC renal failure, nephritis, kidney transplants, toxic or hypoxic
CC injury, neurodegeneration, motor neurone disease, multiple sclerosis
CC bacterial, viral or prion infections (e.g. meningitis, myelopathy
CC associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
CC spinal cord injury, developmental disorders such as Down's syndrome
CC and cerebral palsy, or conditions involving the peripheral nervous
CC system (Lyme disease, muscular dystrophy and myasthenia gravis).
CC Fusion proteins are used to deliver toxins etc. to Ret-expressing
CC cells, especially tumours.

Sequence 464 AA;

Query Match	76.5%;	Score 1788;	DB 28;	Length 464;
Best Local Similarity	56.2%;	Pred. No. 3.78e-158;		
Matches	267;	Conservative 17;	Mismatches 166;	Indels 21;
				Gaps 9;

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Dh 19 slaapslqgdelbgw-pprdvcramelcaaeencsrytllqclagdrnmlan-x 76
Oy 24 ALPLXXxLQeALeGXXKFLXXDcVXXAXXXCAEEXXCSXYYFTLLQCAAGAXXXNTXLASGX 83
Dh 77 e-----cqaaleVlQeapldrcrcrgmkkelqclqyslhlgltegeefyeaspyp 130
Oy 84 EXXXXXXXXXKEXLXXKSLDYDCRCRGOMKEXXCLXIYWSHXHXXLXGNXXLXESPYER 143
Dh 131 -vtarledifflasiifsgtgedpvrvaakshncldaekonldnckllzsyalslcrel 169
Oy 144 XVTSLSDIFEXXKXSKXSKXXDXKXKXSNKCLDPAARCNLMDCKLRSLRYIYXKXKX 203
Dh 190 sptercnrckhkalrqfddrvpseyeyrmlfscsq--dqcaeertrqtl1psscyeke 247
Oy 204 SXHECNRKCKHKLROGFEDKVRPXXHXYGMFLCSCXXXDXACXRRRQTL1PSCSYEXXE 265
Dh 248 kpcncldlrgvcrchlerlcrsladfanacraasyqtvcscpadnyaqclisyagmlgfmtr 307
Oy 264 KPNCLDLRXXKCRTRLXLCBSRLADYXTXCKXXXRVXXSCAXXNYXXCLAAXXGLGTMTPT 323
Dh 308 nyvasaprlgvlspwscgrsgsmeececkrlidftepncrlm1gaifngtdvnpvsgk 367
Oy 324 NYVSSXKTXXXVAARWCRCRSGSGNXXEECEKFLAFXXNPNCLAN1QAFNGXAXXXXXXX 363
Dh 368 --psf-----qa-tqaprvckrlpslddldsdsts1gtsvltctsyqegglkannskel 418
Oy 384 XXPFVSXXKXXXTXTXARVXXPSLXXXXXSKXXLXTYVXXCXLOXOKLKNXSEX 443
Dh 419 smcftelltnlpgsnkvlpknspsrarpasaatlvsymlkal 464
Oy 444 XXCFEELTNNKXXSGXXKXIXXKXXAXPAXLXKLPVLLT-AL 488

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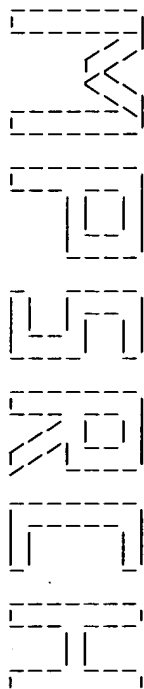
RESULT 5 standard: Protein; 465 AA.

ID W35333; AC W35333; DE 01-MAY-1998 (first entry) DT Human glial cell line-derived neurotrophic factor receptor. KW Human; glial cell line-derived neurotrophic factor; GDNF; receptor; KW treatment; dopaminergic nerve cell disorder; Parkinson's disease; KW Alzheimer's disease; amyotrophic lateral sclerosis; diabetes; KW Huntington's disease; glaucoma; retinal degeneration; hearing loss; KW gene therapy. KW Homo sapiens. PN W09740152-A1. PD 30-OCT-1997. PF 15-APR-1997; U06281. PR 14-APR-1997; US-837199. PR 22-APR-1996; US-015907. PR 09-MAY-1996; US-017221. PA (AMGE-) AMGEN INC. PI Fox GM, Jing S, Wen D; DR N-PSDB: T88419. DR N-PSDB: T88419. PT glial cell line derived neurotrophic factor receptor - useful to PT treat dopaminergic nerve cell disorders, e.g. Parkinson's and PT Alzheimer's disease PS Claim 1; Pages 91-93; 196pp; English. CC The present sequence is the human glial cell line-derived CC neurotrophic factor (GDNF) receptor, which can be used to treat CC dopaminergic nerve cell disorders, e.g. Parkinson's and CC disease or amyotrophic lateral sclerosis, complications of diabetes CC and Huntington's disease and (optionally in combination with GDNF) CC glaucoma, retinal degeneration and hearing loss caused by injury to CC inner ear sensory neurons. The receptor can also be used to block CC unwanted GDNF activity, analyse GDNF related molecules and CC stabilise GDNF in pharmaceutical formulations. Receptor expressing CC cells, preferably transfected ex vivo, can be used similarly by CC implantation, and the use of the receptor cDNA in gene therapy is

CC also contemplated. Probes based on the cDNA can be used to identify
CC GDNF responsive cells and tissues, e.g. to identify patients who
CC would benefit from GDNF therapy, and abnormalities in receptor
CC expression, and to isolate molecules that form a complex with the
CC cDNA or are homologous/cross-reactive with the cDNA. Anti-receptor
CC antibodies, oligonucleotides derived from the cDNA and animal
CC models that overexpress the receptor can be used to study the
CC biological function of GDNF. Knockout transgenic animals can be
CC used to detect GDNF dependent neurons or processes and the antibody
CC can be used in immunoassays for the receptor. The receptor binds
CC GDNF specifically and with high affinity, acting as part of a
CC complex that mediates/enhances signal transduction by GDNF, i.e.,
CC increasing dopamine uptake in dopaminergic cells.

Query Match	76.3%;	Score 1783;	DB 28;	Length 465;
Best Local Similarity	52.8%;	Pred. No. 1.15e-157;		
Matches	255; Conservative	25;	Mismatches 185;	Indels 18;

D	b		1	mfaityfajlpdlallisaevsggdr--dcvksaqdcliegagstkyrrllrvcvaakel	57
Oy		16	MXLVLSLALPLXXXLGLGAEKGXRLXKDCVAXXXCAEXCSXXRYTLRQCXAQXXN	58	
D	b		59	nfsjaegleakde--crsamealpkqslyncrcrkgnmkckekncrlrylwmysiq-oncl	59
Oy		76	NTXLASGEXXXXXXCAXAEXLXSSLYDRCRKRGMKREKXCIXIYWSHXHXXGXGNXX	60	
D	b		116	ledspyeap-vnsrlsdifrvvpifsdvfqgvvehlpkqncldaaacnlddickyrsay	157
Oy		136	LKSPYEPEXYVTSRLSDIFRXKXSXXSXXDXSXXKSNCCLDAAKACNLNDCKKLRSAY	199	
D	b		175	ltpctseavn-dvcnrrrkcbkalqgfcdkvapkhsymlicscer--diacterrqtlyp	233
Oy		196	IYXXXXXXXXKERNRKCHALNQFDKVPXHHXYGMLEFCSCXXDXACKERRORTIXP	255	
D	b		232	vcsyeerekpncnlndgscknyrcrairladffncqgearsvsoclkemypadcllaysy	274
Oy		256	SGSEXXEKKPCDLDRXXKCRTDLCRSRLDFXINCXXXXXXRYASCSAAHYXXCLMAYXG	317	
D	b		292	llgtvmtpnyids-sls-yapwcdansgndleeclklnfkdnltcikaiaqafngs	349
Oy		316	LIGXMPNYVDSSXTXXAVAPMCXCGSGNXMXDECEKFLFXHPNCLANAIQAFCNGX	377	
D	b		350	dvtwtgw---pafrvgttatttaltalrvnkhp-igpagsene-iptchlvpcanlgaki	405
Oy		376	XXXXXXXXXXPFVSXXXXXTXTXAXXVXXPSLXXXXSXKXLLXTVXXKCCXXLOXOL	438	
D	b		404	kansvgnthlcien-gnykegligashttkmaappscgpljlylvrtailstlst	462
Oy		436	KXNKSKXXXXCFEMLTNNXXXXSGXXXXXXIXXXSXAAPSAALXXLPVLMTLALXLSXX	499	
D	b		463	ets 465	
Oy		496	XXS 498		
RESULT	ID		6	w37459 standard; Protein: 460 AA.	
AC			w37459;		
DT			21-MAY-1998 (first entry)		
DE			Human Ret Ligand RetLI.		
KW			Ret ligand; RetLI; receptor; signal transduction; human;		
KW			cell growth; renal cell; nerve cell; renal failure; nephritis;		
KW			kidney transplant; toxic injury; hypoxic injury;		
KW			neurodegeneration; motor neurone disease; multiple sclerosis;		
KW			infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;		
KW			cerebral palsy; Lyme disease; spinal cord injury; Down's syndrome;		
KW			myasthenia gravis; tumour; therapy.		
OS			Homo sapiens.		
PN			M0974J356-A2.		
PD			27-NOV-1997.		
FE			07-MAY-1997;007726.		



(TM)

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March 15 1999 protein - protein database search, using Smith-Waterman algorithm
Run on: Mon Mar 8 14:52:02 1999; Maspar time 24.44 Seconds
763.226 Million cell updates/sec
Tabular output not generated.

Title: >US-08-866-354-43
Description: (1-498) from US08866354.pep
Perfect Score: 2337
Sequence: 1 MVXXLXXXXPPXXXXMLXL.....XLPVLMFLALXLSXXXXX 498

Scoring table: PAM 150
Gap 11

Searched: 116738 seqs, 37463448 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: p1r58
1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 43.709; Variance 79.332; scale 0.551

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	982	42.0	397	2 JE0082	GPI-linked receptor -	4.74e+190
2	108	4.6	493	2 UC5621	epidermal growth fact	7.35e+03
3	108	4.6	2524	2 A35844	Notch protein - Afric	2.04e+02
4	105	4.5	2871	2 A55624	fibrillin-1 precursor	2.85e+02
5	104	4.5	3002	2 A47221	fibrillin I - bovine	5.55e+02
6	102	4.4	2871	2 A55567	HCRF2 protein - human	2.83e+01
7	97	4.2	1121	2 Q01631	hypothetical protein	2.83e+01
8	97	4.2	3051	2 S42373	extracellular protein	5.34e+01
9	96	4.1	387	2 I38449	yBHC protein precursor	9.98e+01
10	95	4.1	427	2 D64813	latent transforming g	9.98e+01
11	96	4.1	1251	2 A56793	epidermal growth fact	9.98e+01
12	93	4.0	469	2 A56918	IDL receptor precursor	7.31e+01
13	93	4.0	530	2 A31640	slit protein 2 precursor	9.98e+01
14	94	4.0	879	1 ORRTD	notch protein homolog	9.98e+01
15	93	4.0	1469	2 B36655	hypothetical 11.6k pr	1.36e+00
16	93	4.0	1480	2 A36655	neurogenic repetitive	1.36e+00
17	93	4.0	2555	2 A40043	fetal antigen 1 - hum	1.36e+00
18	92	3.9	104	2 Q01757	olfactory receptor OR	2.51e+00
19	92	3.9	200	2 A26637	serum albumin - bull	2.51e+00
20	92	3.9	259	2 S48713		
21	92	3.9	260	2 A44549		
22	90	3.9	312	2 S29708		
23	90	3.9	382	2 A37253		

24	92	3.9	383	2 S53716	homeotic protein dlk	1.36e+00
25	92	3.9	383	2 B45484	delta-like dlk homeot	1.36e+00
26	90	3.9	565	1 HNNZC1	hemagglutinin-neurat	2.51e+00
27	91	3.9	826	2 A60385	monocyte surface anti	1.85e+00
28	92	3.9	832	2 A31246	neurogenic protein de	1.36e+00
29	92	3.9	833	2 S19087	gene Delta protein pr	1.36e+00
30	92	3.9	880	2 S00670	gene Delta protein pr	1.85e+00
31	91	3.9	1232	2 D64413	cobalamin biosynthesi	2.51e+00
32	90	3.9	2531	2 S18188	notch protein homolog	1.36e+00
33	92	3.9	2907	2 A57278	fibrillin-2 precursor	1.36e+00
34	92	3.9	2918	2 A54105	fibrillin-2 precursor	1.36e+00
35	89	3.8	249	2 S09868	hypothetical protein	3.39e+00
36	88	3.8	384	2 S25771	gastrin protein - mouse	4.57e+00
37	88	3.8	385	2 A54785	proadipocyte factor 1	4.57e+00
38	89	3.8	509	2 A49664	activin type I recept	3.39e+00
39	89	3.8	603	2 S28941	coagulation factor XI	3.39e+00
40	89	3.8	854	1 ORHTLD	LDL receptor precursor	3.39e+00
41	89	3.8	1013	2 JC2314	chitin synthase (EC 2	3.39e+00
42	89	3.8	1700	2 S08167	Balbiani ring 3 prote	3.39e+00
43	89	3.8	1712	2 A38261	masking protein precu	3.39e+00
44	89	3.8	1810	2 A33230	tenascin precursor -	3.39e+00
45	89	3.8	2471	2 A49128	cell-fate determining	3.39e+00

ALIGNMENTS

RESULT 1
ENTRY 1
TITLE JE0082
ALTERNATE_NAMES GPI-linked receptor - mouse
ORGANISM GPRalpha-3
DATE 21-May-1998 #sequence, revision 29-May-1998 #text_change 24-Sep-1998

ACCESSIONS
REFERENCE JE0082
#authors Nomoto, S.; Ito, S.; Yang, L.X.; Kiuchi, K.
#journal Biochem. Biophys. Res. Commun. (1998) 244:849-853
#title Molecular cloning and expression analysis of GPRalpha-3, a novel cDNA related to GDNFalpha and NTRalpha.

#accession JE0082
#molecule_type mRNA
#residues 1-397 #label NOM
#cross-references DBJ:AB008833; NID:92627159; PID:92627160
COMMENT This protein plays a distinct role in cell survival and differentiation.

KEYWORDS
FEATURE 1-25
380-397
92,145,306
#domain signal sequence #status predicted #label SIG
#region hydrophobic
#binding-site carbohydrate (Asn) (covalent) #status predicted
#length 397 #molecular-weight 44307 #checksum 2962

SUMMARY
Query Match 42.0%; Score 982; DB 2; Length 397;
Best Local Similarity 37.6%; Pred. No. 4.74e+190;
Matches 157; Conservative 41; Mismatches 194; Indels 26; Gaps 19;

DB	3	LSWPPRL-LT-LVLSLWPLG-AGNSLATENRFVNSQTAQRKCEANPACKAAVO 59
OY	5	LKXXPPAPXXMXMLSLALPLXXLQGAELXGXRLXDCVAXXXCXAXCSXXYR 64
DB	60	HUGSCSSLSR--PLPL-BESAMADCELAQAQLNSSLIDRCRHRMKAHQATCDIYWT 116
OY	65	TLRQCKAGXXXTXLSAGEXXXXXCXAXEXLXXSSLYDCRCRGRMKEXXCXIYWS 124
DB	117	VHPARELDYEIDVSPEDVTYSK-P--WKM-NL-SKL--NMLKPD-SDLCIKFAMLCITL 168
OY	125	XHXKXGXMXKXLEKSPYEXYTSRLSDIRXXSXXSXXKXXKXKXKXCDAAKACNL 184
DB	169	HDCKDLRRAYEAC---SGI-RCORHLCTLAQLBSFEKAEASHAOGILLCPACAPEDAG 223
OY	185	NDCKKLRSAVYIXXCXXKXXKXRCNRKRCHALNQFQKVPXHXHYGMLFSCGXKXXXA 244


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Db      224 CERRRNTIAASCAPSV-TNCNDLDSFCRADPLCRSLMDQTCHEPMD-ILIGCATE 281
Oy      245 CERRRQTIITXSCSEEXEKPCNLDLXXCRTDLXCRSLRADYTXCKXXXRVSCAXX 304
Db      282 Q-SRCLRAYLGLIGTAMTPNEI--SKVNTTVALSTCRSGSNLQDCEQLERSFSQNPCL 338
Oy      305 NYXXCLNAXYXGLIGTXMTPNVYDSSTXXXVAFMPCXCRGSNNXKECEKFLKFPFXNPNCL 364
Db      339 VEAIAKARFRHOLFSDQMDSTFSVYQOONSNP-ALRLQPLRPITSEILPILLOT 395
Oy      365 XNAIDAFENGAXXXXXXXXPPFESVXXXXXXTXTXAARVXXX-PSLXXXXXXXLXT 421

RESULT      2
ENTRY        JC5621
TITLE        epidermal growth factor-like protein, T16 - rat
ORGANISM     #formal_name Rattus norvegicus #common_name Norway rat
DATE         09-Oct-1997 #sequence_revision 07-Nov-1997 #text_change
              09-Apr-1998
ACCESSIONS   JC5621
REFERENCE     JC5621
AUTHORS       Ozaki, T.; Kondo, K.; Nakamura, Y.; Ichimiya, S.; Nakagawara,
              A.; Sakiyama, S.
              Biochem. Biophys. Res. Commun. (1997) 237:245-250
              Interaction of D441, a DAN-binding protein, with the
              epidermal growth factor-like protein, S(1-5).
#journal      1-17
#title        #accession JC5621
#molecule_type mRNA
#residues     1-493 #label OZA
#cross-references DBJ:D89730; RID:92429082; PID:d1023127; PID:92429083
COMMENT       This protein plays a role in the regulation of cell growth by
              interacting with DAN protein through D441 protein.
KEYWORDS      glycoprotein
FEATURE       1-17
              28-70,158-199,
              200-237,238-277,
              278-318,319-359
              249
              #domain signal sequence
              #region epidermal growth factor-like repeat\
              #binding_site carbohydrate (Asn) (covalent) #status
              Predicted
              #length 493 #molecular_weight 54596 #checksum 6779

SUMMARY
Query Match      4.6%: Score 108; DB 2; Length 493;
Best Local Similarity 17.5%: Pred. No.7.35e-03;
Matches 10; Conservative 12; Mismatches 34; Indels 1; Gaps 1;

b      156 RIOCAAGYEOSEHNVCODIDECTSGTHNCRLDVNCINLNGSFTGCHCLPEYOKRGBOC 212
Oy      154 RXSXKXKXKXKXKXKXKXKXKXCLDAKACACNLNDCKKLSATITXXKCKXX-SXERC 209

RESULT      3
ENTRY        A35844
TITLE        Xotch protein - African clawed frog
ORGANISM     #formal_name Xenopus laevis #common_name African clawed frog
DATE         12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change
              14-Aug-1998
ACCESSIONS   A35844
REFERENCE     A35844
AUTHORS       Coffman, C.; Harris, W.; Kintner, C.
              Science (1990) 249:1438-1441
              Xotch, the Xenopus homolog of Drosophila notch.
              #cross-references MUID:90385285
#title        #accession A35844
#molecule_type mRNA
#residues     1-2524 #label COF
#cross-references MUID:90385285
COMMENT       preliminary; nucleic acid sequence not shown; not
              compared with conceptual translation

CLASSIFICATION
#molecule_type mRNA
#residues     1-2524 #label COF
#superfamily_unassigned ankyrin repeat proteins; ankyrin
              repeat homology; EGF homology
              transmembrane protein
KEYWORDS      #domain EGF homology #label EGF\
              222-254

```

[illegible]


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Db 308 NYVDSPTGIYVSPMCORSGSNNNEEECKRLRDTFETPPRRRIAIOAFGGNGDIVNNSPKG 367
      ||||| :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Oy 324 NYVDSXTXXYYAAPCMCKRGSGNNXXEECEKRLAFEFXXNPPCLKNIAIOAFGGNXXXXXXXX 363
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 368 --PSF-----QA--QAPRVEKEPSPLPDLSDTSLGTSVTITTTSTVOEGOLKANNSEKEL 418
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Oy 384 XXPXKSVAXXXXXXTXAXRVAVXXSLSLXXXXXXXKXLTXYVAXXXCXHLOXOLKANNSEX 443
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 419 SMCFTELTNTIIPGSNKVIKPNSSPSRRAPSAALTIVLSVLMLOAL 464
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Oy 444 XXCFEELTNTNXXSXXGXXXXXXSXXAXXPSXALXLPVLMLT--AL 488

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ID	RESULT	2	PRELIMINARY:	PRT:	464 AA.
AC	015328				
AC	015328:				
DT	01-JAN-1998	(TREMBLREL. 05, CREATED)			
DT	01-JAN-1998	(TREMBLREL. 05, LAST SEQUENCE UPDATE)			
DT	01-NOV-1998	(TREMBLREL. 08, LAST ANNOTATION UPDATE)			
DE	RET LIGAND 2.				
GN	RETL2.				
OS	HOMO SAPIENS (HUMAN).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUHERIA; PRIMATES;				
CC	CARNARIINI; HOMINIDAE; HOMO.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=LIVER;				
RA	MEDLINE: 97322356.				
RA	SANICOLA M., HESSION C.A., WORLEY D.S., CARMILLO P., EHRENFELDS C.,				
RA	MAIUS L.R., ROBINSON S., JAWORSKI G., WEI H., TIZARD R., WHITTY A.,				
RA	PERPINSKY R.B., CATE R.L.;				
RT	"Glial cell line-derived neurotrophic factor-dependent RET activation				
RT	can be mediated by two different cell-surface accessory proteins.";				
RL	PROC. NATL. ACAD. SCI. U.S.A. 94:6238-6243(1997).				
DR	EMBL: U97145; G2282028; -				
DR	SEQUENCE 464 AA: 51543 MW; 288A8BD8 CRC32;				

Query Match	76.58;	Score 1788;	DB 4;	Length 464;
Best Local Similarity	56.28;	Pred. No. 0.00e+00;		
Matches	262;	Conservative	17;	Mismatches 166;
			Indels	21;
			Gaps	9

[illegible]

RESULT	3		
ID	035977	PRELIMINARY;	PRT: 464 AA.
AC	035977;		
DT	01-JAN-1998 (TREMBLREL, 05, CREATED)		
DT	01-JAN-1998 (TREMBLREL, 05, LAST SEQUENCE UPDATE)		
DT	01-NOV-1998 (TREMBLREL, 08, LAST ANNOTATION UPDATE)		
DE	GNDR CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR-BETA.		
GN	GNDR-BETA OR RETL2.		
OS	RATTUS NORVIGICUS (RAT).		
OC	EUMAROTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA		
OC	SCURIONMTHI; MURIDAE; MURINAE; RATTUS.		

RA TRUPP M, RAYNOSCHER C., IBANEZ C.F. ;
RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN/KIDNEY;
RX MEDLINE: 97322356.
RA NAINICOLA M., HESSON C.A., WORLEY D.S., CARMILLO P., EHRENFELTS C.,
RA MAUS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,
RA PERINSKY R.B., CATE R.L.;
RT "Gial cell line-derived neurotrophic factor-dependent RET activation
RT can be mediated by two different cell-surface accessory proteins." ;
RL PROC. NATL. ACAD. SCI. U.S.A. 94:6238-6243(1997).
RN (3)
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN/KIDNEY;
RA NAINICOLA M., HESSON C.A., WORLEY D.S., CARMILLO P., EHRENFELTS C.,
RA MAUS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,
RA PERINSKY R.B., CATE R.L.;
RL SUBMITTED (APR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF005326. G2323252. -
DR EMBL: U97143. G2282024. -
SO SEQUENCE 464 AA: 51668 MW: BIA2BD11 CRC32:

Query Match	76.4%;	Score 1786;	DB 11;	Length 464;
Best Local Similarity	56.2%;	Pred. No. 0.00e+00;		
Matches	262;	Conservative	19;	Mismatches 164;
			Indels	21;
			Gaps	0;

[illegible]

OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA: RODENTIA:
 OC SCURROGNATHI: MORIDAE: MURINAE: MUS.
 RN [1]
 RC STRAIN-C57;
 RA DEY B. K., MONG Y. W., TOO H. P.;
 RL NEUROREPORT 9:0-0(0001).
 RP SEQUENCE FROM N. A.
 RC STRAIN-C57;
 RA DEY B. K., MONG Y. W., TOO H. P.;
 RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AF015172; G2624963; -
 SO SEQUENCE 463 AA: 51134 MW: 910E17F CRC32:
 Query Match 73.9%; Score 1727; DB 11; Length 463;
 Best Local Similarity 52.1%; Pred. No. 0.00e+00;
 Matches 249; Conservative 29; Mismatches 178; Indels 22; Gaps 14;
 Db 1 MFATLYFVPLDLMNAEVSQDRL--DCYKASDQCLKESQSTKRTLRQCYAGKET 58
 16 MFLALSLALPLXXLLQGAELGXRLXXDCVAXXXCXAEXXCXYRTLRQCGAGXXX 75
 Db 59 NFSLTSGLKAEDE--CRGAEALKOKSLYNCRCRGMKKEKNCLEIYMSMTQSLQ-GNDL 115
 76 NTXLASGEXXXXXXXCAXAXEXLXSSLYDCRCRGMKKEKXCXLIYMSHXHXLXGXGX 135
 Db 116 LEDSEYED-VNSRLSDIFRAVEFISV---EHIS--KGNCLDAKACNLIDTCKKRSAY 169
 136 LEXSPYEPXYTSLRSLDIFRXXSXXSXXXXXXKSNXCILDAKACNLIDCKLRGAY 195
 Db 170 ITPCTSMNSN-EVCCRRCRCHALROFEDKVPKHSYGLFQSCR--DVACIERRQOTIVP 226
 196 IXXCXXXXXXERCNRRCRCHALRQFEDKVPKHXHYGLFQSCXXDXACERERRQOTIXP 255
 Db 227 VCSYERERPNCLNLODSCKTNYICRSRLADFTNCOPESSRSVSNCLKENYADCLLAYSG 286
 256 SCSEYXKRPNCPLDRXXCGRDXLGRSLADFTNCKXXXXXRVYSCAXANXXCLXAXYG 315
 Db 287 LGTVMPTNYIDS-SLS-VAWPCDCSNGDLECLFELNFKDNTCLKNAIQAFNGS 344
 316 LGTMTENYVDSKTXXXVAVPWCXGSGXNXXECCERFLKFXFXNPLXNAIQAFNGX 375
 Db 345 DVTMQRPA--P--PVOTTTATTTTFAIRIKNP-LGPASSENE-ITHTVLPCCANIQAKL 398
 376 XXXXXXXXXXPFSYXXXXXTXAXRVXXPSLXXXXXXLTXVXXCXXLQXQL 435
 Db 399 KSNVSGTHLCLSDNDYGRKDLGASASHITTKSMAPPSGCLSPVAVFTALALLS 456
 436 KXNSXEXXKCPXELTTXKXSGXXXXXXKXAXAPSKALXLPVLTALALLS 493
 RESULT 9
 ID 093512 PRELIMINARY: PRT: 431 AA.
 AC 093512:
 DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE GFR RECEPTOR ALPHA 4 PRECURSOR.
 OS GALLUS GALLUS (CHICKEN).
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: ARCHOSAURIA: AVES:
 OC NEOGNATHAE: GALLIFORMES: PHASIANIDAE: PHASIANINAE: GALLUS.
 RN [1]
 RP SEQUENCE FROM N. A.
 RA MEDLINE: 98313402.
 RA THOMPSON J., DOXAKIS E., PINON L. G., STRACHAN P., BUO-BELLO A.,
 RA WYATT S., BUCHMAN V. L., DAVIES A. M.;
 RT "GFRalpha-4, a new GDNF family receptor";
 RL MOL. CELL. NEUROSCI. 11:117-126(1998).
 DR EMBL: AF045162; G2906032; -
 KW SIGNAL.
 FT SIGNAL. 1 17 POTENTIAL.

FT CHAIN 18 431 GFR RECEPTOR ALPHA 4.
 SO SEQUENCE 431 AA: 47964 MW: 7AE1F0BD CRC32:
 Query Match 52.1%; Score 1218; DB 13; Length 431;
 Best Local Similarity 45.9%; Pred. No. 2.58e-262;
 Matches 157; Conservative 39; Mismatches 132; Indels 14; Gaps 9;
 Db 25 DCLAGSECTNDPICSSKFRTRCICAGNGANK-L--GPDAKNO--CRSYTALLSOLY 79
 45 DCVAXXXCXAEXXCXYRTLRQCGAGXXXNXYLASGEXXXXXXXCAXAXEXXSLY 104
 Db 80 GCKCRGKMKKEKNCLEIYMSIHTLMGEMNVLSESPPEPIRG-F-DYVRLASTAGSEN 137
 105 DCRCKRGMKKEKNCLEIYMSHXHXLXGNXXLESPPEPVATSLSDIFRXXSXXSXXX 164
 Db 138 EVTVGV---NRCLDAKACNDWCORLRTVEYFSCIRRLRADTCNRSCKHAKLRKFPDR 194
 165 DXXXXXKSNXCILDAKACNLIDCKLRSAVIXXXCXXXXXEXERCNRRCRCHALROFEDK 224
 Db 195 VPPEYTHELFQCE--DTCACERRQOTIVPACYSKESKRPNCCLAPDSCHENVVCRSRY 252
 225 VPXXHXHYGLFQSCXXDXACERERRQOTIXPSCYEXXKRPNCCLDRXXCXTDXLGRSL 284
 Db 253 AEFQNCPSLOTASGRBDSYACCLATYGIISPTTPNYIDNS-TSS-IAPCTGNAS 310
 285 ADFXTNCKXXRXVYSCAXANXXCLXAXGLTGMTPVNVDSKTXXXVAVPWCXGRG 340
 Db 311 GNRQECESFLHFTDNCVCLONAIQAFNGTYLNAATPAPIS 352
 345 GNXXECCERFLKFXFXNPLXNAIQAFNGXXXXXXSXXXXX 386
 RESULT 10
 ID 060609 PRELIMINARY: PRT: 400 AA.
 AC 060609:
 DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
 DE GDNF FAMILY RECEPTOR ALPHA 3.
 GN GFR3.
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA: PRIMATIA:
 OC CATARRHINI: HOMINIDAE: HOMO.
 RN [1]
 RP SEQUENCE FROM N. A.
 RA BALOH R. H., GORODINSKY A., GOLDEN J. P., TANSEY M. G., KECK C. L.,
 RA POBESCU N. C., JOHNSON E. M. JR., MILLERADT J.,
 RL PROC. NATL. ACAD. SCI. U. S. A. 0:0-0(1998).
 DR EMBL: AF051767; G2961632; -
 SO SEQUENCE 400 AA: 44538 MW: 6DFB5381 CRC32:
 Query Match 43.9%; Score 1027; DB 4; Length 400;
 Best Local Similarity 37.1%; Pred. No. 4.39e-215;
 Matches 156; Conservative 47; Mismatches 195; Indels 23; Gaps 17;
 Db 1 MYRPLNRPPLPVPVTLMLLLPLPS-PLPLA-AGDPLTESRLNMSCIQARRKCOADPTCS 58
 1 MYXIXLXXXPXPXXMXLXLSTLALPLXXLQGAELGXRLXXDCVAXXXCXAEXXCS 60
 Db 59 AAYVHHLDSCTSI--STPLPS-EEPSVADCLAEAOQLRNSLIGCCHRRMRNOVACLD 115
 61 XXYITLROCAAGXXNXXYLASGAXXXXXXXCAXEXLXSSLYDCRCRGMKEXXCIX 120
 Db 116 IYTVHRAISLGNELVSPYEDTVTSK-P--WRM-NL-SKL--NMLKPD-SDCLKLFAM 167
 121 IYWXKXHXLXXGNXXNXXLESPPEPVATSLSDIFRXXSXXSXXXXXXKSNXCILDAK 180
 Db 168 LCTLNKCDRLKRAYGEC---SGP-HCOHNVCLRLTFPEEAAPRHAGLLCPCAP 222
 181 ACNINLDCCKLRSAVIXXXCXXXXXEXERCNRRCRCHALROFEDKVPKHXHYGLFQSCXX 240
 Db 223 NDRCGERRRNTIAPNCLALPVA--PNCTELRLCFSDPLCRSRVVDOTCHPHMD-ILGT 280

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CC related to native rat GDNFR alpha (see M27327), its variants and
CC soluble derivatives (extracellular domain), chimeric GDNFR alpha
CC and antibodies which bind to the GDNFR alpha, including agonist
CC and neutralising antibodies, as well as various uses for these
CC molecules. It also relates to assay systems for detecting ligands
CC to GDNFR alpha, systems for studying the physiological role of
CC GDNF, diagnostic techniques for identifying GDNF-related conditions
CC methods for identifying molecules homologous to GDNFR alpha, and
CC therapeutic techniques (claimed) for the treatment of GDNF-related
CC and GDNFR alpha-related conditions, particularly kidney disease
CC associated with glomerulonephritis and enteric nervous system
CC related disorders. Transgenic and knockout animals are also
CC claimed.

Query Match	85.0%;	Score 1779;	DB 27;	Length 468;
Best Local Similarity	50.7%;	Pred. No. 2.89e-167;		
Matches 241;	conservative	12;	Mismatches 213;	Indels 9;
				Gaps 8;

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Oy      3 laciylalpbllilmlmsaevsgrdrcdcvkaadqclkgqscstkyrrllrcvgagketnsl 62
Oy      15 LxTLXSLXXPLKLXSSXXXXXXXRDVXAAHXKCAEMXSSXXYYRLRRCAGXAXXNXX 74
Db      63 tsgleakdcrcsramealqkalsyncrcrgmkqkcnclrltysmvsylq-gndlledsy 121
Oy      75 XXXXXAXXAXXAXXEXLXXSSSLYDCRCRKGKKEXXCLXLYWSHXXLLXGXXLEXPY 134
Db      122 e-pvnaieadifrravplisdvfggvnhslygmnldeakcgnlddcckryaayltpctt 180
Oy      135 EXAVTSLRSLDIRRXSSXXSSXXDXDXXXXSSNCKMLDAARACNLNDCKRLRSATYXXCXX 194
Db      181 smsn-evcnrrckhbalqgfdkvpakhysgmjfcscr--diacterrqtlvpycsyee 231
Oy      195 XNXSXCRCRRKCHALRQFEDKVPXHHXYGMLFSCSXDXDAXCERRRQTIPXCSYEX 254
Db      238 reepncslsqdcckenyrcsrriadfftnqgpeersvsnclkenyadclaysgllgtcm 297
Oy      255 XEAPNCLDRISXCRDYDLCRSRLADFXTNCPXRRXXTKXCAAXNYXCCCLAAXXGLIGYM 314
Db      298 tprlydas-sls-varpwcscsngndledclfkfnffkdnctclkaiaqfngsgdvrmwq 355
Oy      315 TPRYVDSXKTXKXVAPKXCRGSGNXXEBCBKLXAFXXNPLCLXNLIQAFCGADVYKMSQ 374
Db      356 paprpvqtatcttafrvknhr-tpagseneipr-thvlppcanlpaqklksnvsgrthl 413
Oy      375 XXPXXXXTXAXXXXXXXRXVXXPLXKXXSXSSXXXTYVXXXCXXXXOXQLKXNXSXXXX 434
b      414 clsdedfgcdgagssnhltkmaapppscslslylmntalaalvswlaets 468
Oy      435 CAXXXXXXXXXXXXXXXXXXXXXXKXXLXXLPVLLIYKLLXXKXXLXXKXLETS 489

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RESULT	2
ID	W35334 standard; Protein; 468 AA.

DE 01-MAY-1998 (first entry)
DT rat glial cell line-derived neurotrophic factor receptor.
KW Rat; glial cell line-derived neurotrophic factor; GDNF; receptor;
KW treatment; dopaminergic nerve cell disorder; Parkinson's disease;
KW Alzheimer's disease; amyotrophic lateral sclerosis; diabetes;
KW Huntington's disease; glaucoma; retinal degeneration; hearing loss;
KW gene therapy.
OS Rattus sp.
PN MO9740152-41.
PD 30-OCT-1997.
PE 15-APR-1997; U06281.
PR 14-APR-1997; US-83719.
PR 22-APR-1996; US-015907.
PR 09-MAY-1996; US-017221.
PA (AMGE-) AMGEN INC.
PI Fox GM, J'ing S, Wen D;
DR WPI: 97-535836/49.
DR N-PSDB: T95297.

Pt G1a1 cell line derived neurotrophic factor receptor - useful to
 Pt treat dopaminergic nerve cell disorders, e.g. Parkinson's and
 Pt Alzheimer's disease
 Pt Claim 1; Pages 96-98; 16pp; English.
 P5 The present sequence is the rat G1a1 cell line-derived
 CC neurotrophic factor (GDNF) receptor, which can be used to treat
 CC dopaminergic nerve cell disorders, e.g. Parkinson's and Alzheimer's
 CC disease or anyotropic lateral sclerosis, complications of diabetes
 CC and Huntington's disease and (optionally in combination with GDNF)
 CC glaucoma, retinal degeneration and hearing loss caused by injury to
 CC inner ear sensory neurons. The receptor can also be used to block
 CC unwanted GDNF activity, analyse GDNF related molecules and
 CC stabilise GDNF in pharmaceutical formulations. Receptor expressing
 CC cells, preferably transfected *ex vivo*, can be used similarly by
 CC implantation, and the use of the receptor cDNA in gene therapy is
 CC also contemplated. Probes based on the cDNA can be used to identify
 CC GDNF responsive cells and tissues, e.g. to identify patients who
 CC would benefit from GDNF therapy, and abnormalities in receptor
 CC expression, and to isolate molecules that form a complex with the
 CC cDNA or are homologous/cross-reactive with the cDNA. Anti-receptor
 CC antibodies, oligonucleotides derived from the cDNA and animal
 CC models that overexpress the receptor can be used to study the
 CC biological function of GDNF, knockout transgenic animals can be
 CC used to detect GDNF dependent neurons or processes and the antibody
 CC can be used in immunoassays for the receptor. The receptor binds
 CC GDNF specifically and with high affinity, acting as part of a
 CC complex that mediates/enhances signal transduction by GDNF, i.e.
 CC increasing dopamine uptake in dopaminergic cells.
 P9 Sequence 468 AA;

Query Match	85.08;	Score 1779;	DB 28;	Length 468;
Best Local Similarity	50.78;	Pred. No. 2.89e-167;		
Matches	241;	Conservative	12;	Mismatches 213;
			Indels	9;
			Gaps	8;

Dd	3	laelyfalplldlmsaeavgddrldcvkaadqclbqsgcstkyrrllrqcvagketnsl	62
Qy	15	lxlrlxlaaplrlkxssxxxxxxkdxvaykaxxkmaexkssxyrrlrbckagxxxxxxx	74
Dd	63	tsglaeckscraemaalkqkalyncrcrkgmkxekncrlrywamyqlq-gndlledsy	122
Qy	75	xxxxxxxscxxaxekxlxxsslydpcrcrgmkexkxclxywshxxlxxgxxxlexsp	133
Dd	122	e-pyuarlledfravpflsdrfgqvshstsgmncldaeakcnlddcckkyzaaytptct	180
Qy	135	expvtrlsbdrfrxxssxxxxxxdxxxxxxsnckcladaakcnlndckkrlrsaytlykcx	193
Dd	181	smen-ewcnrrckhalkrqfdkvpahhsygmjfcscr--dlactetrtrqtlvprvcye	239
Qy	195	xxsxmxrcmrckrckhalknqpfedkvpxxhxygmfcscxxhdacxkrrrogtlpxpcstex	256
Dd	238	repcnclsldgdcctnyrcsrsladfltnccqpesrsvnckenyadcllaysgllqtw	297
Qy	255	xexpcncldrscrcrdxlcrsrladpftynccpxpxrxxtkcaxkxnyxcclaxvxcglctxm	314
Dd	298	tpnyvds-sls-vapwcdsngndledcklfnnfkndhtclknlaefgngsdvrtmw	355
Qy	315	tpnyvdsxttxxxavpocxcrgsgnxxebecfkllaxfxnnpclxnltqofgsgdvxmasq	372
Dd	356	pappvgtattatcttafrvknhr-lpagsaselnr-ctvlrpccanlqacklksnysqschl	413
Qy	375	xxexxxxttxxxkxxxrxyxxpxlxxxxsxxxxxtxvxxcxkxqxlkxkxssxxxx	432
Dd	414	clsdadefgdcagasshltckmaapscselslylmaltalaalvslaets	469
Qy	435	cxkxxxxxxxxxxxxxxxxxxxxxxkaxxxsxxlxxlplmltlylxxlxxlxxlxxl	489

RESULT 3
W37457 standard; Protein; 468 AA

DT 21-MAY-1998 (first entry)
DE Rat Ret ligand RetL.
KW Ret ligand; RetL; receptor; signal transduction; rat;

KM	cell growth; renal cell; nerve cell; renal failure; nephritis;
KW	kidney transplant; toxic injury; hypoxic injury;
KW	neurodegeneration; motor neurone disease; multiple sclerosis;
KW	infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
KW	cranial nerve injury; spinal cord injury; Down's syndrome;
KW	cerebral palsy; Lyme disease; muscular dystrophy;
KM	myasthenia gravis; tumour therapy.
OS	Rattus sp.
FH	Key
FT	Peptide
FN	Location/Qualifiers
PD	1..24
PV	/label=Sig_peptide
PF	M09744356-A2.
PR	27-NOV-1997.
PR	07-MAY-1997.
PR	10-APR-1997.
PR	08-MAY-1996.
PR	07-JUN-1996.
PR	16-JUL-1996.
PA	(BIOJ) BIOGEN INC.
PI	Cate RL, Hesston C, Santicola-Nadel M,
DR	WPI: 98-018431/02.
N-PSDS:	V00245.
PT	New nucleic acid encoding ret receptor ligands and related proteins
PT	- vectors, transformed cells and antibodies, used for promoting cell
PT	growth and improving survival of injured cells, especially renal or
PT	nerve cells
PS	Claim 2: Page 49-51. 113pp. English.
CC	This protein comprises rat Ret ligand (RetL) RetL, a key component
CC	of the Ret signalling pathway that specifically interacts with Ret
CC	receptor protein, triggering Ret dimerisation and/or
CC	autophosphorylation of the Ret tyrosine kinase domain. The amino
CC	acid sequence was deduced from a cDNA clone (see V00245) obtained
CC	from a rat embryonic kidney cDNA expression library. Human RetL
CC	as well as mouse and human RetL2 and RetL3 sequences have also been
CC	identified (see W37458-63). Vectors containing retL DNA and
CC	prokaryotic or eukaryotic host cells transformed or transfected
CC	with these vectors are claimed, as well as a method for production
CC	of RetL, its soluble variants (e.g. amino acids 1-434) and fusion
CC	proteins with a toxin, imageable compound or radionuclide. RetL,
CC	optionally when expressed from vectors in vivo, is used to promote
CC	growth of new tissue and survival of damaged tissue, particularly
CC	kidney or neural tissue. Typical applications are in renal failure,
CC	nephritis, kidney transplants, toxic or hypoxic injury,
CC	neurodegeneration, motor neurone disease, multiple sclerosis,
CC	bacterial, viral or prion infections (e.g. meningitis, myelopathy
CC	associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
CC	spinal cord injury, developmental disorders such as Down's syndrome
CC	and cerebral palsy, or conditions involving the peripheral nervous
CC	system (Lyme disease, muscular dystrophy and myasthenia gravis).
CC	Fusion proteins are used to deliver toxins etc. to Ret-expressing
CC	cells, especially tumours.
SO	Sequence 468 AA;
Query Match	85.0%; Score 1779; DB 28; Length 468;
Best Local Similarity	50.7%; Pred. No. 2,896-167;
Matches 241; Conservative	12; Mismatches 213; Indels 9; Gaps 8
Dd	3 lacyfalfplldlmnseavsggdridcvtkaadqqlkegscstkyrtlrvgavgctetfsf 62
Oy	15 LXTLTLSEXXPLXLLXXXSXXXXXXDCVAXXXCXAEXKSCSXRYRTLTQCAAGAXNXXNX 74
Dd	63 tsgleakdecrsamaalqkqslayncrcrgmkheknclirlysmwygsq_ gndlleds py 121
Oy	75 XXXXXAAXXECXAXXKLXSSLYPCRCRKRGAKKEVXCXLITWSXHXKLXAXXXLEASPY 134
Dd	122 e-pvnrsrdsdfiravpfisdvfvqvehsksgnncldaecaenldctckxyrsayltpctt 180
Oy	135 EXPVTSRLSDIFRXSXSXSXXXXXDXSXXSKCLDAKAACNLNDXCKRKLRSAVITXXCX 194
Dd	161 smsn-evcnrrtkchkalngffdkvpakhsygmflfsc--dlacterrrrgtlpyvcysge 237
Oy	195 XKSXKERCNRRKCHALNQFDKPXKHXYGMLFCSCKXDXDACKERRRQTITXSCSTEX 254

Db 238 renoiclsqskctyicrsrladffincpgpsrsvsnclkeypadc1laysg1l9tcm 297
| | | | | : | : | : | | | | | | | | | | | | | | | | | | | | | | | |
Oy 235 XEPLPCDLRXXCCTDXLCRSRLADFTNCKPXXRXXTXCAKNVXXCLANVXGLTGTXM 314
Db 298 tpryvds-sjs-vapwcdcsngndledclkfinfkdnctclnaelqafongsdvcmwq 305
| | | | | : | : | : | | | | | | | | | | | | | | | | | | | | | | | |
Oy 315 TPNTYDASXXTXAXAPMCXCNGSGSNXXEECEKFLMXFXNNPCLNMAIQAOTGNGADVAMNSQ 312
Db 336 pappvqttaacttaafvknp-1gpagseuefp-thvlppcanlgaqlksnvsstll 1
Oy 375 XXPPXXXXTXAXXXXXXRFXXXFPXLXXXXXSTYVVXXXXCXHXQXOLTKNXSAXAXXA 2
Db 414 clsdgsdfgkgdlaagasshltksmappaescslspjlmhtalaa1lsvsaets 140
Oy 435 CXXXXXXXXXXXXXXXXXXXXXXXXXSLXLPVLMLTRTLXNLXNLXNLXETS 489

RESULT 4
ID M37460 standard; Protein: 464 AA.
AC M37460;
DC 21-MAY-1998 (first entry)
DE Human Ret Ligand RetL2.
KW Ret ligand; RetL; RetL2; receptor; signal transduction; human;
KW cell growth; renal cell; nerve cell; renal failure; nephritis;
KW kidney transplant; toxic injury; hypoxic injury;
KW neurodegeneration; motor neurone disease; multiple sclerosis;
KW intracranial meningitis; myelopathy; Creutzfeldt-Jakob disease;
KW cranial nerve injury; spinal cord injury; Down's syndrome;
KW cerebral palsy; Lyme disease; muscular dystrophy;
KW myasthenia gravis; tumour; therapy.
OS Homo sapiens.
PN MO9744356-A2.
PD 27-NOV-1997.
PE 07-MAY-1997; U07726.
PR 10-APR-1997; US-017427.
PR 08-MAY-1996; US-017427.
PR 07-JUN-1996; US-019300.
PR 16-JUL-1996; US-021859.
PA (BIOJ) BIOGEN INC.
PI Cate RL, Hession C, Sanicola-Nadel M;
DR WPJ: 98-018431/02.
DR N-PDSB: V00248.
PT New nucleic acid encoding ret receptor ligands and related proteins
PT - vectors; transformed cells and antibodies, used for promoting cell
PT growth and improving survival of injured cells, especially renal or
PT nerve cells
PS Claim 2; Page 69-70; 113pp; English.
CC This amino acid sequence comprises human Ret ligand (RetL) RetL2,
CC deduced from a cDNA clone (see V00248) isolated from a human foetal
CC liver library. Rat and human RetL2 and human and mouse RetL3
CC sequences (see W3757-59 and W37461-63) are also claimed. Human
CC RetL2 is 49.1% identical to human RetL1 protein. RetL is a
CC key component of the Ret signalling pathway that specifically
CC interacts with Ret receptor protein, triggering Ret dimerisation
CC and/or autophosphorylation of the Ret tyrosine kinase domain.
CC Vectors containing retL2 DNA and prokaryotic or eukaryotic host
CC cells transformed or transfected with these vectors are claimed, as
CC well as a method for production of RetL2, its soluble variants and
CC fusion proteins with a toxin, imageable compound or radionuclide.
CC RetL2, optionally when expressed from vectors in vivo, is used to
CC promote growth of new tissue and survival of damaged tissue.
CC particularly kidney or neural tissue. Typical applications are in
CC renal failure, nephritis, kidney transplants, toxic or hypoxic
CC injury, neurodegeneration, motor neurone disease, multiple sclerosis
CC bacterial, viral or prion infections (e.g. meningitis, myelopathy
CC associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
CC spinal cord injury, developmental disorders such as Down's syndrome
CC and cerebral palsy, or conditions involving the peripheral nervous
CC system (Lyme disease, muscular dystrophy and myasthenia gravis).
CC Fusion proteins are used to deliver toxins etc. to Ret-expressing
CC cells, especially tumours.
SQ Sequence 464 AA;

Query Match 84.5%; Score 1768; DB 28; Length 464;
 Best Local Similarity 53.3%; Pred. No. 3,906-166;
 Matches 244; Conservative 14; Mismatches 187; Indels 13; Gaps 4;

DB 16 tlrtaapsqgdpelngwppvdcvranelaesncsrrytlrqlgldnrlm-- 73
 17 tlrtaapsqgdpelngwppvdcvranelaesncsrrytlrqlgldnrlm-- 76
 74 ---ankcgaalevlgdsgpdydcrcckgmkkelqclqlyslhlylgegeefyaape- 129
 77 XXXXXKXXAXEXLXXSSSLYDCCKGKMKEXXCLXIVSXHXLLXGXXYLEXSPYEX 136
 DB 130 pvtisldftrlaeliffgtagdqvvsakshcldaekacnldncklrssylscrel 189
 137 PVTISLDFIRXXSXSSXXXDXDXXXXKXNXCDAAKACNLNDCKLRSAVITXXCXXX 196
 DB 190 spcerctrrckhalrffirvpeaytylmfscq--dqaacerrtqlipscsyedke 247
 197 SXXERCRRRCHALRQFFPKVPXHXHYGMLFCSCXXXDXACXERRQITXPCSYEXXE 256
 DB 248 kpnclldrgvcrthlcrsladfhancrsyqtvtscpdnygaclgsyagmldfcmtp 307
 257 XPNCLDRSCRTDXLCRSLADFTNCPXKXHXKXAXXKXCLXAXYXGLIGTXMP 316
 DB 308 nyvdasptglvswpcscrgsgmmeceekfirdfencplrnaigaftgndvnyspk 367
 317 NYVDSXXTXXVAPWCRCRSGSXNHECEKFLXXFXNPNCLNNAIAGFNGXVXMSQXX 376
 DB 368 pafwqatqep-----rvckpslpddlsdstslsvltctsvqegglkxmskelsmf 422
 377 PAXXXXTXAXXXXXRXVXXFXLXXXXSXSSXXXTYVXXKXXQXOLKXNXXSXXXXXC 436
 DB 423 teltlnlpgsnkvlpkpsgrsarpaaaltvsvlm 460
 437 XXXXXXXXXXXXXXXXXXXXXSXXAXXXLXLPVLM 474

RESULT 5
 ID W35333 standard; Protein: 465 AA.
 AC W35333;
 DT 01-MAY-1998 (first entry)
 DE Human glial cell line-derived neurotrophic factor receptor.
 KW Human; glial cell line-derived neurotrophic factor; GDNF; receptor;
 KW treatment; dopaminergic nerve cell disorder; Parkinson's disease;
 KW Alzheimer's disease; amyotrophic lateral sclerosis; diabetes;
 KW Huntington's disease; glaucoma; retinal degeneration; hearing loss;
 KW gene therapy.
 OS Homo sapiens.
 SN W09740152-A1.
 PD 30-OCT-1997.
 PF 15-APR-1997; U06281.
 PR 14-APR-1997; US-837199.
 PR 22-APR-1996; US-015907.
 PR 09-MAY-1996; US-017221.
 PA (AMGE-) AMGEN INC.
 PI Fox GM, Jing S, Wen D;
 DR WPI; 97-535836/49.
 DR N-PSDB; T88419.
 PT Glial cell line derived neurotrophic factor receptor - useful to
 treat dopaminergic nerve cell disorders, e.g. Parkinson's and
 Alzheimer's disease
 PT Claim 1: Pages 91-93; 196pp; English.
 CC The present sequence is the human glial cell line-derived
 CC neurotrophic factor (GDNF) receptor, which can be used to treat
 CC dopaminergic nerve cell disorders, e.g. Parkinson's and Alzheimer's
 CC disease or amyotrophic lateral sclerosis, complications of diabetes
 CC and Huntington's disease and (optionally) in combination with GDNF)
 CC glaucoma, retinal degeneration and hearing loss caused by injury to
 CC inner ear sensory neurons. The receptor can also be used to block
 CC unwanted GDNF activity; analyse GDNF related molecules and
 CC stabilise GDNF in pharmaceutical formulations. Receptor expressing
 CC cells, preferably transfected ex vivo, can be used similarly by
 CC implantation, and the use of the receptor cDNA in gene therapy is

CC also contemplated. Probes based on the cDNA can be used to identify
 CC GDNF responsive cells and tissues, e.g. to identify patients who
 CC would benefit from GDNF therapy, and abnormalities in receptor
 CC expression, and to isolate molecules that form a complex with the
 CC cDNA or are homologous/cross-reactive with the cDNA. Anti-receptor
 CC antibodies, oligonucleotides derived from the cDNA and animal
 CC models that overexpress the receptor can be used to study the
 CC biological function of GDNF. Knockout transgenic animals can be
 CC used to detect GDNF dependent neurons or processes and the antibody
 CC can be used in immunoassays for the receptor. The receptor binds
 CC GDNF specifically and with high affinity, acting as part of a
 CC complex that mediates/enhances signal transduction by GDNF, i.e.
 CC increasing dopamine uptake in dopaminergic cells.
 SQ Sequence 465 AA;

Query Match 81.0%; Score 1695; DB 28; Length 465;
 Best Local Similarity 49.5%; Pred. No. 1,236-158;
 Matches 235; Conservative 17; Mismatches 211; Indels 12; Gaps 10;

DB 3 latlialpdlldlssaevsgdrldcvkaadqclkegscstkyrtlqcvagketnfa 72
 15 LXTLXSLXPLXLLXSSXXSXXSXXDCVAXXXCAEXXCSXXYRLRQCXAGXXNXX 74
 DB 63 aaglleakdecrsamealkqslyncrctrgmkcknclriysmyqslq-gndlledsqy 121
 75 XXXXXAXXKXXAXEXLXXSSSLYDCCKRGMKEXXCLXIVSXHXLLXGXXYLEXSPY 134
 DB 122 e-pvnsrladfrvvpflsadvfgvehlpkgncldaekacnlddckkyrsayltptcl 160
 135 EXPVTSRLSDIRRXSXSSXXSXXSXXKXNXCDAKACNLNDCKLRSAVITXXCXX 194
 DB 181 svsn-dvencrrckhalrffirvpeaytylmfscq--dqaacerrtqlipscsyee 237
 195 SXXERCRRRCHALRQFFPKVPXHXHYGMLFCSCXXXDXACXERRQITXPCSYEX 254
 DB 238 repnclldgdccknyrcrsladfhancrsyqtvtscpdnygaclgsyagmldfcmtp 297
 255 XPNCLDRSCRTDXLCRSLADFTNCPXKXHXKXAXXKXCLXAXYXGLIGTXM 314
 DB 298 tpylidas-sls-vapwcdsngndleclkfinafkancilksaigaftgndvnyspk 355
 315 TPNYVDSXXTXXVAPWCRCRSGSXNHECEKFLXXFXNPNCLNNAIAGFNGXVXMSQ 374
 DB 366 pafwqatqatcttalrknkp-tpagsenelp-thvlpcanlgaqklksnysgnthl 413
 375 XXPXXXTXAXXXRXVXXFXLXXXXSXSSXXXTYVXXKXXQXOLKXNXXSXXX 434
 DB 414 clsnngyekelgashltcr-smaappscglapllvltvralstlls--ltets 465
 435 CXXXXXXXXXXXXXXXXXXXXSXXAXXXLXLPVLMXLLXLLXLETXS 489

RESULT 6
 ID W37459 standard; Protein: 460 AA.
 AC W37459;
 DT 21-MAY-1998 (first entry)
 DE Human Ret Ligand RetL.
 KW Ret ligand; RetL; receptor; signal transduction; human;
 KW cell growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury;
 KW neurodegeneration; motor neurone disease; multiple sclerosis;
 KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
 KW cranial nerve injury; spinal cord injury; Down's syndrome;
 KW cerebral palsy; Lyme disease; muscular dystrophy;
 KW amyotrophic lateral sclerosis; tumour; therapy.
 OS Homo sapiens.
 SN W09744356-A2.
 PD 27-NOV-1997.
 PF 07-MAY-1997; U07726.
 PR 10-APR-1997; US-017427.
 PR 08-MAY-1996; US-017427.
 PR 07-JUN-1996; US-019300.
 PR 16-JUL-1996; US-021859.


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OY 309 LGTMTPTVYDSXXTXVAPMCKRGSGNXXECEKFLXXFXNPLXNMQFGNXX 368
DB 231 dttvqpaipvtctatttalttrvknkp-1gpaageneip-thv1ppcan1aqk1ksnv 288
OY 369 DVMXSOQXXXXXXXTXAXXXXXXXRVXXXPYXXXXXXSXXXXXXVXXXCXQXQXKXNX 428
DB 289 sgnthtclsnngykeqeglgashtctk-smaapscglp1lv1vtaltstlls--1let 345
OY 429 SXXXXXXCXXXXXXSXXXXXXSXXXXXXSXXXXXXSXXXXXXSXXXXXXSXXXXXX 488
DB 346 s 346
OY 489 S 489

RESULT 8
ID W37461 standard; Protein: 397 AA.
NC W37461;
NC 21-MAY-1998 (first entry)
E Mouse Ret. ligand RetL3.
KW Ret. ligand; RetL; RetL3; receptor; signal transduction; mouse;
KW cell growth; renal cell; nerve cell; renal failure; nephritis;
KW kidney transplant; toxic injury; hypoxic injury;
KW neurodegeneration; motor neurone disease; multiple sclerosis;
KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
KW cranial nerve injury; spinal cord injury; Down's syndrome;
KW cerebral palsy; Lyme disease; muscular dystrophy;
KW myasthenia gravis; tumour; therapy.
OS Mus musculus.
PN WO9744356-A2.
PD 27-NOV-1997.
PF 07-MAY-1997; U07726.
PR 10-APR-1997; US-017427.
PR 08-MAY-1996; US-017427.
PR 07-JUN-1996; US-019300.
PR 16-JUL-1996; US-021859.
PA (BIOJ) BIOGEN INC.
PI Cate RL, Hession C, Santicola-Nadel M;
PI WPI: 98-018431/02.
DR N-PSDB; V00249.
PT New nucleic acid encoding ret receptor ligands and related proteins
PT - vectors, transformed cells and antibodies, used for promoting cell
PT growth and improving survival of injured cells, especially renal or
PT nerve cells
PS Claim 2: Page 77-78; 113pp; English.
NC This amino acid sequence comprises mouse Ret ligand (RetL) RetL3,
NC deduced from cDNA clones (see V00249) isolated from an EST
NC database and by 5'RACE. Rat and human RetL1, human RetL2 and RetL3
NC sequences (see W37457-60 and W37462-63) are also claimed. RetL is
NC a key component of the Ret signalling pathway that specifically
NC interacts with Ret receptor protein, triggering Ret dimerisation
NC and/or autophosphorylation of the Ret tyrosine kinase domain.
NC Vectors containing RetL DNA and prokaryotic or eukaryotic host
NC cells transformed or transfected with these vectors are claimed, as
NC well as a method for production of RetL3, its soluble variants and
NC fusion proteins with a toxin, imageable compound or radionuclide.
NC RetL3, optionally when expressed from vectors in vivo, is used to
NC promote growth of new tissue and survival of damaged tissue.
NC Particularly kidney or neural tissue. Typical applications are in
NC renal failure, nephritis, kidney transplants, toxic or hypoxic
NC injury, neurodegeneration, motor neurone disease, multiple sclerosis,
NC bacterial, viral or prion infections (e.g. meningitis, myelopathy
NC associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
NC spinal cord injury, developmental disorders such as Down's syndrome
NC and cerebral palsy, or conditions involving the peripheral nervous
NC system (Lyme disease, muscular dystrophy and myasthenia gravis).
NC Fusion proteins are used to deliver toxins etc. to Ret-expressing
NC cells, especially tumours.
SQ Sequence 397 AA;

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Query Match 46.7%; Score 976; DB 28; Length 397;
 Best Local Similarity 40.4%; Pred. NO. 3.53e-85;

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Matches 143; Conservative 35; Mismatches 157; Indels 19; Gaps 1.
DB 10 p1m1111v1w1p1p1gag1natentfvnsc1qarkkceanpckaaqy1hscets1s 69
OY 10 PXXXXLXTLXSLXPLXMXSXXXXXXRXDXDCVAXXXCMAEXXCSXXRYRTLROCKXGX 69
DB 70 rplpleesamaa-dcleaeq1lms1ldcrchrnmkqgctld1wvhpars1gdyel 126
OY 70 XNXXXXXXAXXEXCAXXEXLXSSLYDCCKRGKMKEXXCLTIYXSXHXLXGXAXL 129
DB 129 dvsyedtvtak-p--vkm-n1-skl--nm1kpd-sd1cl1fam1ct1hkc1d1lxrayg 180
OY 130 EXPYEXPVTSRLSDIFRXSXXSXXSXXSXXSXXSXXSXXSXXSXXSXXSXXSXXSXX 189
DB 181 eac-----sgt-rqqrh1claq1rfefekaaeshag1llcpapedagcgerrnt1aps 235
OY 190 XXXXXXXXXEXRCNRKMKALROFFDKVPYXXHYGMLFCSCXXXDXNACXBRRO1T1PS 249
DB 236 calpsv-tpncld1rsfcradp1crsr1mdftqchpmd1lgt-cateq-src1ray1gl 292
OY 250 CYEXXEXPNCLDRSKCRTXILCRSLADPXTMCXPXRXXTYCXAXNXXCX1A1X1XGL 309
DB 293 1gtamtgnfiskvnt--val1sc1crsgn1qdeceq1ersfsgnplvea1aa 344
OY 310 IGTMTPTVYDSXXTXVAPMCKRGSGNXXECEKFLXXFXNPLXNMQFGNXX 363

RESULT 9
ID W37463 standard; Protein: 400 AA.
NC W37463;
NC 21-MAY-1998 (first entry)
DE Human Ret. ligand RetL3.
KW Ret. ligand; RetL; RetL3; receptor; signal transduction; human;
KW cell growth; renal cell; nerve cell; renal failure; nephritis;
KW kidney transplant; toxic injury; hypoxic injury;
KW neurodegeneration; motor neurone disease; multiple sclerosis;
KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
KW cranial nerve injury; spinal cord injury; Down's syndrome;
KW cerebral palsy; Lyme disease; muscular dystrophy;
KW myasthenia gravis; tumour; therapy.
OS Homo sapiens.
PN WO9744356-A2.
PD 27-NOV-1997.
PF 07-MAY-1997; U07726.
PR 10-APR-1997; US-017427.
PR 08-MAY-1996; US-017427.
PR 07-JUN-1996; US-019300.
PR 16-JUL-1996; US-021859.
PA (BIOJ) BIOGEN INC.
PI Cate RL, Hession C, Santicola-Nadel M;
PI WPI: 98-018431/02.
DR N-PSDB; V00251.
PT New nucleic acid encoding ret receptor ligands and related proteins
PT - vectors, transformed cells and antibodies, used for promoting cell
PT growth and improving survival of injured cells, especially renal or
PT nerve cells
PS Claim 2: Page 85-86; 113pp; English.
NC This amino acid sequence comprises human Ret ligand (RetL) RetL3,
NC deduced from cDNA clones (see V00251) isolated from a adult heart
NC and spinal cord libraries. Rat and human RetL1, human RetL2 and
NC mouse RetL3 sequences (see W37457-62) are also claimed. Human
NC RetL3 is 34.3% identical to human RetL1, 34.9% identical to human
NC RetL2 and 76.8% identical to murine RetL3. Ret ligand is a key
NC component of the Ret signalling pathway that specifically
NC interacts with Ret receptor protein, triggering Ret dimerisation
NC and/or autophosphorylation of the Ret tyrosine kinase domain.
NC Vectors containing RetL DNA and prokaryotic or eukaryotic host
NC cells transformed or transfected with these vectors are claimed, as
NC well as a method for production of RetL3, its soluble variants and
NC fusion proteins with a toxin, imageable compound or radionuclide.
NC RetL3, optionally when expressed from vectors in vivo, is used to
NC promote growth of new tissue and survival of damaged tissue,
NC particularly kidney or neural tissue. Typical applications are:

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CC renal failure, nephritis, kidney transplants, toxic or hypoxic
CC injury, neurodegeneration, motor neurone disease, multiple sclerosis,
CC bacterial, viral or prion infections (e.g. meningitis, myelopathy
CC associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
CC spinal cord injury, developmental disorders such as Down's syndrome
CC and cerebral palsy, or conditions involving the peripheral nervous
CC system (Lyme disease, muscular dystrophy and myasthenia gravis).
CC Fusion proteins are used to deliver toxins etc. to Ret-expressing
CC cells, especially tumours.
SQ Sequence 400 AA;

Query Match 44.5%; Score 931; DB 28; Length 400;
Best Local Similarity 36.4%; Pred. No. 1,29e-80;
Matches 142; Conservative 43; Mismatches 185; Indels 20; Gaps 14;

Db 18 ||||ppppllaagdpplpsteerlmnsclqarrkqadpccsaayhnlscscslst-plp 76
OY 15 LXTLKSLLXPLXLLXSSXXXKXDXVAXXKXAEKXXKXXYFTLQCAKAGXKXNXX 74
Db 77 seepvpadclaaagqlnssllgcmehrmkngvacldiyvtvtrarslgnylevdepy 136
OY 75 XXXXAXXEXCXXAXEXLXSSLYDCRCRGMKEXXCLXITVSHXHLXKXGXXLEKSPY 134
Db 137 edtvsk-p--wkm-nl-skl--nmkpd-sdlclkfamclctndkcdrlrkaygeac-- 186
OY 135 EXPVTSRLSDIFRXXSXXXSXXSXXSXXSXXSXXSXXSXXSXXSXXSXXSXXSXXSXX 194
Db 187 --sgp-hqgrhvcrlqlltfekaeahagqlllpcapndgceerrntlapncalpp 243
OY 195 XXXXRECRNRKCHALRQFEDKVPXHXHYGMLFCSCXXDXKXERRQRTXPSCSYEX 254
Db 244 va-pncldlrlcfdsrslvdqfchbmdllgt-cateq-srclraylgltgntam 300
OY 255 XEPCDLRSKCRIDXLCSRHLADFTXNCXPRXXKXHXKXAXXKXCLXKXGLIGTXM 314
Db 301 tnfsvsnvts--valsectrgsgnlgcecemlegfshnpclteaakmfhaqlfsq 358
OY 315 TPNVDSXXTXVAPMCCRCGSGNXXECCERFLKXXFXNPLXNALQAFGNGXVXXSQ 374
Db 359 dwpbptfavmahqenpavirpqpwpisfs 388
OY 375 XXXPXXXTX-AXXXXXXVXXPXXLXXXX 403

RESULT 10
ID W37465 standard; Protein: 346 AA.
AC W37465;
DT 21-MAY-1998 (first entry)
DE Mouse Ret ligand RetL3 partial sequence.
KW Mouse RetLigand; RetL3; receptor; signal transduction; mouse;
KW cell growth; renal cell; nerve cell; renal failure; nephritis;
KW kidney transplant; toxic injury; hypoxic injury;
KW neurodegeneration; motor neurone disease; multiple sclerosis;
KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
KW cranial nerve injury; spinal cord injury; Down's syndrome;
KW cerebral palsy; Lyme disease; muscular dystrophy;
KW myasthenia gravis; tumour; therapy.
OS Mus musculus.
PN W09744356-A2.
PD 27-NOV-1997.
PF 07-MAY-1997; U07726.
PR 10-APR-1997; US-017427.
PR 08-MAY-1996; US-017427.
PR 07-JUN-1996; US-019300.
PR 16-JUL-1996; US-021859.
PA (BioU) BIOGEN INC.
PI Cate RL, Hession C, Sanicola-Nadel M;
DR WPI: 98-018431/02.
DR N-PSDB: V00256.
PT New nucleic acid encoding ret receptor ligands and related proteins
PT - vectors, transformed cells and antibodies, used for promoting cell
PT growth and improving survival of injured cells, especially renal or
PT nerve cells

PS Disclosure: Page 73-74; 113pp; English.
CC This polypeptide comprises a partial sequence of mouse Ret ligand
CC RetL3, deduced from EST AA050083 cDNA (see V00256). A full-length
CC mouse RetL3 sequence (see W37465) was also obtained. Rat, mouse
CC and human RetL3, RetL2 and RetL3 cDNA sequences (see V00245-51) and
CC encoded polypeptides (see W37457-63) are claimed and can be used
CC in methods for promoting cell growth and improving survival of
CC cells, especially renal or neural cells.
SQ Sequence 346 AA;

Query Match 41.2%; Score 861; DB 28; Length 346;
Best Local Similarity 45.2%; Pred. No. 1,35e-73;
Matches 127; Conservative 29; Mismatches 107; Indels 18; Gaps 12;

Db 31 dclaaagqlnssllgcmehrmkngvacldiyvtvtrarslgnylevdepydvtvsk- 76
OY 83 ECKXAXEXLXSSLYDCRCRGMKEXXCLXITVSHXHLXKXGXXLEKSPYEXPVTSRL 142
Db 90 p--wkm-nl-skl--nmkpd-sdlclkfamclctndkcdrlrkaygeac---sgl- 186
OY 143 SDIFRXXSXXXSXXSXXSXXSXXSXXSXXSXXSXXSXXSXXSXXSXXSXXSXXSXXSXX 203
Db 138 qhlcqlqslsfekaeahagqlllpcapndgceerrntlapncalpsv-tpncl 243
OY 203 NRRKCHALRQFEDKVPXHXHYGMLFCSCXXDXKXERRQRTXPSCSYEXEXPNCID 312
Db 197 lrsferadpdlrslmdqfchbmdllgt-cateq-srclraylgltgntamtnflskv 254
OY 263 LRSXCRIDXLCSRHLADFTXNCXPRXXKXHXKXAXXKXCLXKXGLIGTXMTPNVDX 322
Db 255 ntt--valsectrgsgnlgdeceqlersfsgnplveaiaa 293
OY 323 XTXXVAPMCCRCGSGNXXECCERFLKXXFXNPLXNALQAFGNGXVXXSQ 374

RESULT 11
ID W37462 standard; Protein: 315 AA.
AC W37462;
DT 21-MAY-1998 (first entry)
DE Human Ret ligand RetL3 partial sequence.
KW Human RetLigand; RetL3; receptor; signal transduction; human;
KW cell growth; renal cell; nerve cell; renal failure; nephritis;
KW kidney transplant; toxic injury; hypoxic injury;
KW neurodegeneration; motor neurone disease; multiple sclerosis;
KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
KW cranial nerve injury; spinal cord injury; Down's syndrome;
KW cerebral palsy; Lyme disease; muscular dystrophy;
KW myasthenia gravis; tumour; therapy.
OS Homo sapiens.
PN W09744356-A2.
PD 27-NOV-1997.
PF 07-MAY-1997; U07726.
PR 10-APR-1997; US-017427.
PR 08-MAY-1996; US-017427.
PR 07-JUN-1996; US-019300.
PR 16-JUL-1996; US-021859.
PA (BioU) BIOGEN INC.
PI Cate RL, Hession C, Sanicola-Nadel M;
DR WPI: 98-018431/02.
DR N-PSDB: V00250.
PT New nucleic acid encoding ret receptor ligands and related proteins
PT - vectors, transformed cells and antibodies, used for promoting cell
PT growth and improving survival of injured cells, especially renal or
PT nerve cells
PS Claim 2; Page 81-82; 113pp; English.
CC This amino acid sequence comprises a human Ret ligand (RetL) RetL3
CC partial polypeptide sequence, deduced from a partial clone (see
CC V00250) isolated from a human adult heart cDNA library; a
CC full-length RetL3 sequence (see W37463) is also claimed, as well
CC as rat and human RetL1, human RetL2 and mouse RetL3 sequences
CC (see W37455-61). Ret ligand is a key component of the Ret
CC signalling pathway that specifically interacts with Ret receptor
CC protein, triggering Ret dimerisation and/or autophosphorylation of

CC the Ret tyrosine kinase domain. Vectors containing retL3 DNA and
 CC prokaryotic or eukaryotic host cells transfected or transfected
 CC with these vectors are claimed, as well as a method for production
 CC of RetL3. Its soluble variants and fusion proteins with a toxin,
 CC imageable compound or radionuclide. RetL3, optionally when
 CC expressed from vectors in vivo, is used to promote growth of new
 CC tissue and survival of damaged tissue, particularly kidney or
 CC neural tissue. Typical applications are in renal failure,
 CC nephritis, kidney transplants, toxic or hypoxic injury,
 CC neurodegeneration, motor neuron disease, multiple sclerosis,
 CC bacterial, viral or prion infections (e.g., meningitis, myelopathy
 CC associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
 CC spinal cord injury, developmental disorders such as Down's syndrome
 CC and cerebral palsy, or conditions involving the peripheral nervous
 CC system (Lyme disease, muscular dystrophy and myasthenia gravis).
 CC Fusion proteins are used to deliver toxins etc. to Ret-expressing
 CC cells, especially tumours.
 SQ Sequence 315 AA;

Query Match 38.2%; Score 799; DB 28; Length 315;
 Best Local Similarity 40.1%; Pred. No. 2,81e-67;
 Matches 126; Conservative 34; Mismatches 135; Indels 19; Gaps 13;

DB 8 lrrssllgcmchrnmknqvacldlyvtharslgnelydvspdyetvsk-p-wkm-n 63
 QY 91 LKXSSLYDCRCKRGMKEXXCLXIYWSXHXLLXGXGXXLEXPYETVRLSDIFRXXS 150
 DB 64 L-SKL--nmklkpd-sdclclfamclctlnckcdllrkaygac-----sgp-hcqrhncrlq 114
 QY 151 XNXXXXXXDXNXXKXNKLDAARACNLDXCKRLRSAYIYXCCXXXSXXECCNRRCCKHA 210
 DB 115 llffekaeephaqglllpcapndrgcgrrrntlapncalpvpa-pnclelrrlcfqd 173
 QY 211 LRQFDFKVPKXHXHYGMFCSCXXXDXACXERRQITXPCSYEXXKXEPNCLDRSKCRTD 270
 DB 174 plcrsr-lvdfqthcnpmldlgt-cateq-srclraylglgtamcpnfsvnvt--val 229
 QY 271 XLCRSRLAFXTNCKXPXRXRXTCXANXXCLAXYGLIGTXYMTPYVDSXXTXXVAP 330
 DB 230 sctcrgsgnlqecemlegffshnpcltealeakmrfhsqldfsgdphnftfawmaqn 289
 QY 331 WCACRGSGNXXECCERFLXKXFXNPNCLXNAIQFNGXGDVXMQXPPXXXXTX-AAxxxx 389
 DB 290 pavrpgwvpslfs 303
 QY 390 XRYXXXPLXKXKS 403

RESULT 12
 ID R94563 standard; Protein: 1810 AA.
 AC R94563;
 DT 21-JUN-1996 (first entry)
 DE Chicken cytotactin.
 KW Cytotactin; neuron; neurite; cell attachment; cell elongation;
 KW fibronectin.
 OS Gallus sp.
 FH Key
 FT region location/Qualifiers
 FT 1..591
 FT /note= "EGF-like repeat region"
 FT 592..773
 FT /note= "fibronectin type III repeats I-II"
 FT 774..864
 FT /note= "fibronectin type III repeat III"
 FT 865..956
 FT /note= "fibronectin type III repeat IV"
 FT 957..1044
 FT /note= "fibronectin type III repeat V"
 FT 1318..1398
 FT /note= "fibronectin type III repeat VI"
 FT 1045..1317
 FT /note= "alternatively spliced fibronectin type
 FT III repeat VAVDVC"
 FT 1132..1569
 FT region

FT /note= "fibronectin type III repeats VII and
 FT VIII (lacking 13 N-terminal amino acids)"
 FT 1318..1398
 FT /note= "fibronectin type III repeats III-VI"
 FT 1570..1810
 FT /note= "fibronogen domain plus fibronectin type
 FT III repeat VIII N-terminalus"
 PN W09608513-A1.
 PD 21-MAR-1996.
 PF 14-SEP-1995; 011684.
 PR 16-SEP-1994; US-308359.
 PA (SCRI) SCRIPPS RES INSTR.
 PI Crossin KL, Phillips G, Prieto AL;
 DR WPI: 96-179904/18.
 DR N-PSDB; T14548.
 PT Cytotactin polypeptide(s), derivs. and antibodies - capable of
 PT stimulating neuronal cell attachment, neurite out-growth and cell
 PT elongation
 PS Claim 9; Page 118-126; 159pp; English.
 CC Chicken cytotactin (R94563) and human cytotactin (R94562) are
 CC multidomain extracellular matrix proteins capable of stimulating
 CC neuronal cell attachment, neurite outgrowth and cell elongation.
 CC The cytotactins, or functional portions of them (see R94564-69),
 CC can be obtd. by expression of encoding DNA (see T14548 and
 CC (T14547) in host cells, e.g. as GST fusion proteins in Escherichia
 CC coli. They have therapeutic and diagnostic applns. and can be
 CC used to raise antibodies.
 SQ Sequence 1810 AA;

Query Match 4.6%; Score 96; DB 16; Length 1810;
 Best Local Similarity 24.3%; Pred. No. 7.44e+00;
 Matches 25; Conservative 18; Mismatches 49; Indels 11; Gaps

DB 185 pncs-epacpncln-rglcvrakclceegfgedsgarcpdcndggkcvdgv-cvcf 241
 QY 248 PSCSYEXXKXEPNCLDRSXC-RTDXLCRSRLA--D-FXTNCKPXXRXHXTCXAXNXXCL 303
 DB 242 egyptgdcgeelcph--gcsghlrgcvggrcvche-gfgedcn 281
 QY 304 KAYXGLI-GTXMTPNVDSXXTXXVAPWCXCRGSGNXXECC 345

RESULT 13
 ID R56166 standard; Protein: 383 AA.
 AC R56166;
 DT 26-JAN-1995 (first entry)
 DE Neuroendocrine tumor dlk.
 KW Dlk; neuroendocrine tumor; monoclonal antibody.
 OS Homo sapiens.
 FH Key
 FT peptide location/Qualifiers
 FT 1..23
 FT /label= Sig_peptide
 FT 62
 FT /label= N-myristylation_site
 FT 72
 FT /label= N-myristylation_site
 FT 100
 FT /label= N-glycosylation_site
 FT 101
 FT /label= N-myristylation_site
 FT 109
 FT /label= N-myristylation_site
 FT 120
 FT /label= protein-kinase-C-phosphorylation_site
 FT 187
 FT /label= hydroxylation_site
 FT 288
 FT /label= protein-kinase-C-phosphorylation_site
 FT 302
 FT /label= protein-kinase-C-phosphorylation_site
 FT 312
 FT /label= N-myristylation_site
 FT 312
 FT /label= N-myristylation_site
 PN W09413701-A.

Release 3.1A John F. Collins, Biocomputing Research Unit
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MPsrch_pp    protein - protein database search, using Smith-Waterman algorithm
Run on:      Mon Mar  8 15:04:28 1999;    MasPar time 23.89 Seconds
Tabular output not generated.             766.704 Million cell updates/sec

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Description: (1-489) From US08866354.pep
Perfect Score: 2092
Sequence: 1 XXXXXXXXXXXXXLTLS.....PYLMTLXLLXLLXLLXETS 489
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Scoring table: PAM 150
Gap 11

Searched: 116738 seqs, 37463448 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 42.322; Variance 73.547; scale 0.575

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description	Pred. No.
1	976	46.7	397	2	JE0082	GPI-linked receptor -	3.04e-19
2	108	5.2	493	2	U55621	epidermal growth fact	1.82e-03
3	109	5.2	2524	2	A35844	Xotch protein - Atfic	1.26e-01
4	108	5.2	3002	2	AA7221	fibrlin1 precursor	1.82e-03
5	107	5.1	2871	2	A55567	fibrlin1 - bovine	2.62e-03
6	105	5.0	2871	2	A55624	fibrlin1 - precursor	5.38e-03
7	96	4.6	387	2	I38449	extracellular protein	1.25e-01
8	96	4.6	1810	2	A32230	tenascin precursor -	1.25e-01
9	94	4.5	570	2	A48836	fibropellin C	2.44e-01
10	94	4.5	879	1	ORR1TD	LDL receptor precursor	2.44e-01
11	95	4.5	1232	1	D64413	cobalamin biosynthesis	1.75e-01
12	94	4.5	1700	2	S08167	Balbin1 ring 3 prote	2.44e-01
13	95	4.5	2531	2	A46019	gene Notch-1 protein	1.75e-01
14	94	4.5	2555	2	A40043	notch protein homolog	2.44e-01
15	92	4.4	259	2	S48713	fetal antigen 1 - hum	4.74e-01
16	92	4.4	260	2	A44549	fetal antigen 1 homeo	4.74e-01
17	92	4.4	383	2	B45484	delta-like dlx homeot	4.74e-01
18	92	4.4	383	2	S53716	homeotic protein dlx	4.74e-01
19	92	4.4	469	2	A56918	farnesoid x-activated	3.41e-01
20	93	4.4	2703	2	A24420	notch protein - fruit	4.74e-01
21	92	4.4	2907	2	A57278	fibrlin1-2 precursor	4.74e-01
22	92	4.4	2918	2	A54105	fibrlin1-2 precursor	4.74e-01
23	89	4.3	200	2	A26633	neurogenic repetitive	1.26e+00

25	89	4.3	249	S09868	hypothetical protein	1.26e+00
24	89	4.3	385	D568780	dopamine D1-like rece	1.26e+00
26	90	4.3	427	D64813	Ybnc protein precursor	9.12e-01
24	89	4.3	511	S44275	coagulation factor pro	1.26e+00
28	89	4.3	603	S28941	coagulation factor XI	1.26e+00
27	89	4.3	826	A60385	monocytic surface anti	6.59e-01
30	89	4.3	854	1 ORHYD	LDL receptor precursor	1.26e+00
31	89	4.3	1712	S43261	masking protein precu	1.26e+00
32	90	4.3	3051	S82373	hypothetical protein	9.12e-01
33	89	4.3	5147	1 JUEFM	cadherin-related immo	1.26e+00
34	88	4.2	293	B26637	neurogenic repetitive	1.73e+00
35	87	4.2	385	A54785	preadipocyte factor 1	2.38e+00
36	87	4.2	385	S23718	homeotic protein dlx	2.38e+00
37	87	4.2	903	S60327	homeotic protein alpha	2.38e+00
38	88	4.2	1203	A49175	Motcn B protein - mou	1.73e+00
39	87	4.2	1251	A57293	latent transforming g	2.38e+00
40	88	4.2	2139	A57672	crumbs protein - firl	1.73e+00
41	88	4.2	3069	H70656	probable fcs protein	1.73e+00
42	86	4.1	370	B43306	Dnrf - Streptococys p	3.26e+00
43	86	4.1	832	A31246	neurogenic protein De	3.26e+00
44	86	4.1	886	A57172	probable hormone rece	3.26e+00
45	86	4.1	972	A50363	glycoprotein GP350, r	3.26e+00

ALIGNMENTS

RESULT	1	JEO082	#type complete
ENTRY		GPI-linked	receptor - mouse
TITLE		Gpralpha-3	
ALTERNATE_NAMES		#formal_name Mus musculus	#common_name house mouse
ORGANISM		21-Mar-1998	#sequence_rev1ston 29-May-1998
DATE		24-Sep-1998	#text_change

ACCESSIONS
REFERENCE

#authors Nomoto, S.; Ito, S.; Yang, L.X.; Kiuchi, K.
#journal Biochem. Biophys. Res. Commun. (1998) 244:849-853
#title Molecular cloning and expression analysis of GFRalpha-3,
novel cDNA related to GDNFRalpha and NTRalpha.
#accession JE0082.

```
##mO
##re
```

#cross-references DDBJ:AB008833; NID:G2627159; PID:G26271600

COMMENT This protein plays a distinct role in cell survival and differentiation.

KEYWORDS

1-25	#domain signal sequence	#status predicted	#label signal
380-397	#region hydrophobic\		
92,145,306	#binding site carbohydrate (Asn)	(covalent)	#status

SUMMARY

Query Match	46.78;	Score 976;	DB 2;	Length 397;
Best Local Similarity	40.48;	Pred. No. 3,04e-198;		
Matches 143; Conservative	35;	Mismatches 157;	Totals 10;	Cases 14

10	INITIATIVE	20	CONSERVATIVE	30	MISMANICLED	40	INUENTS	50	VALP
----	------------	----	--------------	----	-------------	----	---------	----	------

[illegible]

09 PAAAAATLTLASLAAFLALAAASAAAAAAAAAACDCVAAAAAACAEEAKCSAAI KILRQCAKXON

```

DB      /0 RPLLEESANSA-DCELEAEQLRNSSLIDPCRRKRRKQCATCELDYIWIIVHPARSLCQYI
      : : | | | | | | | | | | : | | | | |

```

```
09 /XXXXXXXXXXAXXECXXXXEXLXSSTDCRCRKGKREXCETIYWSHXHXLXGXXLL L.
```

Db 129 DVSPEEDTWSK-P--WKN-NL-SKL--NMLKPD-SDCLKFAIMCTLHDKCBRLKAYG 181

QY 130 EASPYEXPVTSRLSDIFRAXSXSXSXXDXDXXXXXSXCLDAACNCLNDXCRLRSAYI 189

[illegible]

Qy 190 XXXXXXXXXERCNRRKCHALRQFEDKVPXXHHXGMLFCSCXXXDXACXERRQITXPS 249


```

2057-2089          #domain ankrylin repeat homology #label ANS
SUMMARY            #length 2524 #molecular-weight 274931 #checksum 9441

Query Match      5.2%; Score 109; DB 2; Length 2524;
Best Local Similarity 16.0%; Pred. No. 1,266-03;
Matches 26; Conservatve 18; Mismatches 109; Indels 10; Gaps 10;

Db    1150 SPNPGNGATGCTDYLGGVSCCEGVAAHYHGVNCSEELNECLSPICONGGCIDILITTYCSC 1209
      :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY    44 AAXXXCAEXXCSXXRTTLR-QCKAAXX-NMXXXXXXXAXXECXXAXEXLXSSLYCCRC 101
      :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB    1210 PRG-TGVHC-EIN-VDDCTPFPSDFLTPEPKCNNGKCIDRVG-YNCI-CPGFVGERC 1264
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY    102 KRGKREKXXCLAIYMSXHXLLXGXHHLEXPYEKP-VTSLSDIFRXSXSSXXDXDX 160
      ::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db    1265 EGD-VNECLSNPCDSRGTCNQICQLVNDYRCRCRGQFTGR-RCE 1305
      ::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY    161 XXXKSXNKCIDAAKACNLNDXCKRLRSAYIXXKXXXXXSXCERN 203
      ::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||

RESULT 4
ENTRY   4                                     #type fragment
TITLE   fibrillin I precursor - human (fragment)
ORGANISM HUMAN
DATE .
ACCESSIONS
REFERENCE
#authors Corson, G.M.; Chabberg, S.C.; Dietz, H.C.; Charbonneau, N.L.
#journal Genomics (1993) 17:476-484
#title Fibrillin binds calcium and is coded by cDNAs that reveal a multidomain structure and alternatively spliced exons at the 5' end.
#accession A47221
##molecule_type mRNA
##residues 1-337,'T',339-1029 ##label COR
##cross-references GB:X63556
REFERENCE
#authors Perletti, L.V.; D'Alessio, M.; Ramirez, F.; Lynch, J.; Sykes, B.; Pangillman, T.; Bonadio, J. Hum. Mol. Genet. (1993) 2:961-968
#title The genomic organization of the sequence coding for fibrillin, the defective gene product in Marfan syndrome.
#cross-references MIMD:93372860
#accession I54355
##status Preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues 132-3002 ##label PER
##cross-references GB:L13923; NID:g306745; PID:g306746
REFERENCE
#authors Maslen, C.L.; Corson, G.M.; Maddox, B.K.; Glenville, R.W.; Sakai, L.Y.
#journal Nature (1991) 352:334-337
#title Partial sequence of a candidate gene for the Marfan syndrome
#accession S17064
##molecule_type mRNA
##residues 1030-3002 ##label MAS
##cross-references EMBL:X63556
REFERENCE
#authors Dietz, H.C.; Valle, D.; Francomano, C.A.; Kendzior, R.J. Science (1993) 259:680-683
#title The skipping of constitutive exons in vivo induced by nonsense mutations.
#cross-references MIMD:93157831
#accession I59574
##status Preliminary; translated from GB/EMBL/DBJ
##molecule_type DNA
##residues 2217-2288,'T',2290-2325 ##label RES
##cross-references GB:S54426; NID:g264860; PID:g264861
REFERENCE
#authors Lee, B.; Godfrey, M.; Vitale, E.; Hort, H.; Mattei, M.G.; Sartorelli, M.

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```

Db 74 ---NKNEQOALLEYQSPDYDRCRCRGMKKELOQOIQIYWSIHLGTEGEEPEYEAPE- 129
Oy 77 XXXXXHECXAXXEXLXXSSSLDYDRCRCRGMKKEKXCXLIYWSHXHXXLXGXXHLESPYEX 136
Db 130 PVTSRLSDIFRLASIFSGTGTPDAVSTKSNHCLDAAKACNLNDNCKRLRSSYISICNEI 189
Oy 137 PVTSRLSDIFRXHXSXSSXXXDXDXXXXXXSXVCLDAAKACNLNDXCKRLRSAYIXCXXXX 196
Db 190 SPTSRCNRRCRCHALRQFEPFRVPSEYTYRMLTCSQO--DQACERRQOTILPSCSYEDEK 247
Oy 197 SXMRCCNRRCCHALRQFEPFRVPSXXXHXGLFCSCXXXMXACXERRQTIAPSCSYEXXE 256
Db 248 KPNCLDLSRLCTDHLCLRSRLADFPANHCBSASYRTITSCPADYVQACLSYAGMIGFDMTP 307
Oy 257 XPNCLDLSRGNCRDYLCLRSRLADFPXNCKAPXXRXXTXCKAXNYXXCLAYYGLIGTXMTP 316
Db 308 NYVDSNPTGIIVSPWCNCRGSGMNEECCERFLRDFTEPNCLRNALIOAFNGSTDVNMSPKG 367
Oy 317 NYVDSXXTXXXVAPWCNCRGSGNXXEECEERFLXFXFXNPNCLRNALIOAFNGCXDVYMSGXX 376
Db 368 PSLPAPQAP-----RVEKTPSLPDDLSDBSTSLGTSYITTCISIQDQGLKANNSELSMCF 422
Oy 377 PXXXXXTAXXXXXXXRXVXXXPXLLXXXXSXXXXXXXTXVXXXCXXOXOXLKRXNXXSXXXXXX 436
Db 423 TELFTNISPGSKRYIKLNGSGSRARLSALTPALPLMLT 461
Oy 437 XXXXXXXXXXXXXXXXXXXXXSXXAXXSXLLXLPVLMLT 475

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RESULT	2	PRELIMINARY:	PR:	464 AA.
ID	015328			
AC	015328:			
DT	01-JAN-1998	(TREMBLREL, 05, CREATED)		
DT	01-JAN-1998	(TREMBLREL, 05, LAST SEQUENCE UPDATE)		
DT	01-NOV-1998	(TREMBLREL, 08, LAST ANNOTATION UPDATE)		
DE	RET LIGAND 2.			
GN	RET12.			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA: PRIMATES			
OC	CATARRHINI: HOMINIDAE: HOMO.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-LIVER:			
RX	MEDLINE: 97322356.			
RA	SANICOLA M., HESSION C. A., WORLEY D. S., CARMILLO P., EHRENFELDS C.,			
RA	WALUS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,			
RA	PEPINSKY R. B., CAPE R. L.,			
RT	“clial cell line-derived neurotrophic factor-dependent RET activation			
RT	can be mediated by two different cell-surface accessory proteins.”;			
RL	PROC. NATL.ACAD.SCI. U.S.A. 94:6238-6243(1997).			
EMBL	U57145; G2282028; -			
QO	SEQUENCE 464 AA: 51543 MW; 288A8BD8 CRC32;			

Query Match	84.58;	Score 1768;	DB 4;	Length 464;
Best Local Similarity	53.38;	Pred. No. 0.00e+00;		
Matches	244;	Conservative	14;	Mismatches 187;
			Indels	13;
			Gaps	4

Db	16	TLRSLAPSSJLOGELHGMRPVPCVANELCAAESNCSRRYLRLROCLAGROBNTML--	73
Qy	17	TLSLAXPLALXAXXXXXXXRXKXDXADCVAXXXXXCAEXXCSXXYRFLRLQCKXGXXXXXX	76
Db	74	--ANKEQCALLEVLOESPLYDCRCRCKRGMRKELOCLQIYWSIHGLTGEGBFEYASYE-	129
Qy	77	XXXXXXECXAXXEXLXXSSLYDCRCRCKRGMRKEXXCLTIYWSKHXKLLXGXXKXLESPYEX	136
Db	130	PVTSRLSDIRLRLSIFSGTGADPVVSAKSKSNHCLDAAACNLNDCKFLRSSYISICNREI	189
Qy	137	PVTSRLSDIRRXXSXXSXXXXXXKSKSNXCDDAAACNLNDCKFLRSAYIYXXCXXXX	196
Db	190	SPTERCRRRCCHALRQFEDRPVSEYIYRMLFSCQ--DQACAERRQTLPLPSCSYDKE	247
Qy	197	SXXERCRRRCCHALRQFEDRPVPEXXHXIGMLFSCQXXXXDACKERRRQTLIYPCSCSYEXE	256

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Db      248 KPNCLDLRGVCRTHLCRSRLADHANCRASTQVTSCPADNYOACIGTAGMIGFPM") 307
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      257 XPCNCLDSKRCORTDYLCSRRLADEXTXCCPXXRRXXTXCKAAXYXXCLAAVXGLGTMYTP 316
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      308 NYVDSSPYGIIVSPMCSCRSGSNGNEEDECERFLRDPFTENPCLRNAIQAFGNTDVNVSPKG 367
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      317 NYVDSXMTXXXVAAPCMCROSGSNGNXEEBCEKFLAXFXKNPCLXNAINQAFGNGXDVMXSQXX 376
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      368 PSFQATQP-----RVEXTPSLPDDLSDSTSLSGTSVTTTCTSVOEGLKANNSKELSMCF 422
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      377 PAXXKTAKXXXXXXRXVXXXPFLIXXXSXXXXXXJTVXXXCXKXOXQLKXNKSXXXXXXCX 436
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      423 TELTNIIPGSNKRIKPNCSGRARPSALATVLVSLEML 460
          | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy      437 XXXXXXXXXXXXXXXXXXXXSKXMAKSKXLXLPVLEL 474

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RESULT	3	PRELIMINARY;	PRT;	464 AA.
ID	015316			
AC	015316;			
DT	01-JAN-1998 (TREMBLREL. 05, CREATED)			
DT	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)			
DT	01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)			
DE	GIJAL CELL LINE-DERIVED NEUROTROPIC FACTOR RECEPTOR BETA.			
GN	GNFR-BETA.			
OS	HOMO SAPIENS (HUMAN).			
OS	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES			
OC	CATARRHINI; HOMINIDAE; HOMO.			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=FETAL BRAIN;			
RA	MARTIOVARA K., SUVANTO P., HORELLI-KUITUNEN N., LINDAHL M.,			
RA	MOSHNYAKOV M., AIKASINEN H.S., PALOTIE A., SARIOLA H., SAARMA M.;			
RL	SUBMITTED (MAR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.			
DR	EMBL: U93703; G2228737;			
SO	SEQUENCE	464 AA;	51530 MW;	DE80D543 CRC32;

Query Match	84.5%;	Score 1768;	DB 4;	Length 464;
Best Local Similarity	53.3%;	Pred. No. 0.00e+00;		
Matches	244;	Conservative	14;	Mismatches 187;
			Indels 13;	Gaps 4

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Db 16 TLTSLASPSSLOGPHELHGMPVPCVANELCAEANSCSSRRPTLROCLAGDRBTML - 73
Qy 17 TLASLAKPLALXKASXXXXXXRXDXCQVAXAXXCAEXXCXNYHTLROCAAGAXXXXXX 76
Db 74 ---ANKFCAALEVLOESPPLYDCRCRGRMKRELQLOIYWSIHLGLTEEEFEYASPYE- 129
Qy 77 XXXAXECCXXAEXXELXSLSDYDCRCRGRMKREXXCLXIYWSXHXLLXGXXLXEPSYEX 130
Db 130 PYTSRLSDIEFLASLFFSTGADPYVSAKSHHCDAACNLNDNCKRLRSYISICNBEI 169
Qy 137 PYTSRLSDIEFLKXSXSXSXSXSXSXSXSXSXSXCDAKACNLNDCKRLRSAYIXXCXXX 199
Db 190 SPTEHCNRKCHKALROFFDVPSEYTYRYMLFSCSCQ--COACAERROTILPSCSYEDKE 247
Qy 197 SXHERCNRRKCHKALROGFVDPVXXHXYGMLFSCSXKXDXACKERRROTIPSCSYEXXE 255
Db 248 KPCICDLRGVCTDHLCLSLADBFHANGCRASYOTVTSCPADNYOACLCISVAGMIGFDMTP 307
Qy 257 XPCICDLRGVCTDHLCLSLADBFHTXTCXKXKXKXCAKAXNYXCCLAYGLIGTMYPT 314
Db 308 NYVDSPPGIYVSPMCSRGSGNMEECCEKFLDFTENPCLNNAIOAGNCTDVPVSPKG 367
Qy 317 NYVDSXITXXAAVAPMCACRGSGNAXEECEFFLXXFXFNACLNNAIOAGNCDVVMQOXX 370
Db 368 PSEOATQAP-----RVKETSPLPDDLSDSYISLGTSYITTCVSQEOGLKANNSKELSMCF 422
Qy 377 PXXXTTAXAXXXXXXXRVXXXP LXKXXXXX XXXXXXTYVXXXCXGXQXQLKXNXSXXXXXGX 437
Db 423 TELTITNIIPGSKVYIKPNSGSPRRRPSALITVLSVMTL 460
Qy 437 XXXXXXXXXXXXXXXXXXXXXXXXKXAXXSXLLXJLXPVMTL 474

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RESULT 4 PRELIMINARY; PRT: 468 AA.

AC 035246; (TREMBLEREL. 05, CREATED)

DT 01-JAN-1998 (TREMBLEREL. 05, LAST SEQUENCE UPDATE)

DT 01-JAN-1998 (TREMBLEREL. 05, LAST SEQUENCE UPDATE)

DE GENE RECEPTOR ALPHA.

OS GDNF-ALPHA.

OS MUS MUSCULUS (MOUSE).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;

OC SCIUROGNATHI; MORIDAE; MORINAE; MUS.

RP SEQUENCE FROM N.A.

RC STRAIN-C57; TISSUE-LIVER;

RA DEY B.K., MONG Y.W., TOO H.P.;

RL NEUROREPORT 9:0-0(0001).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-C57; TISSUE-LIVER;

RA DEY B.K., MONG Y.W., TOO H.P.;

RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: AF014117; G2624961; -

SO SEQUENCE 468 AA; 51751 MW; AFDC6A1 CRC32;

Query Match 84.2%; Score 1762; DB 11; Length 468;

Best Local Similarity 49.7%; Pred. No. 0.00e+00;

Matches 236; Conservative 19; Mismatches 211; Indels 9; Gaps 8;

Db 3 LATLYFVLPDLILMSAEVSGDRDLCVAKASDCLKEGSCSTKYRTLROCVAGKETFNLSL 62

Qy 15 LXTLSLXPLXLLXSSXXXXXXDCVAXXXCXAEXXCSXXRTLRQCGAGXXXXXX 74

Db 63 TSGLEAKDECRSAMEALOKSLYNCRCRGMKREKNCILRIYMSYSLQ-GNDLLEDSPY 121

Qy 75 XXXXXAXXEXXAXEXLXSSLYDCRCKRMKREKXCLXIYWSYXXLXGXGXXLXSPY 134

Db 122 E-PVNSRLSDIFRAVPEISV--EHIS--KGNCLDAKACNLDTCCKYRSAYITPCTT 180

Qy 135 EXPVTSRLSDIFRAXXSSXXXXXXKSNCLDAKACNLDCKRLRSATIXXXCX 194

Db 181 SMSN-EVCNRRKCHKALROFEDKVPARKSYGMFCSCR--DIACERRRQTIIVPCSYEE 237

Qy 195 XXSXXERCNRRKCHKALROFEDKVPXHXGYGMLFCSCXXMXACKERRRQTIIVPCSYEX 254

Db 238 RERNCLNLDSCKTNYICRSRLADFTNCOPEBSRVSNCLEKENYADCLLAYSGLIGTVM 297

Qy 255 XEHPNCLDLRSXCRTDYLCSRLADFTNCPXXXRXXTXCAAXNYXXCLXAYXGLIGTVM 314

Db 298 TPNTIDSS-SLS-VAPMCDSCNSGNDLEDCLKFLNFNDNTCLNNAIOAFNGSDVTMMQ 355

Qy 315 TPNTVDSXXTXVAPMCDSCNSGNDLEDCLKFLNFNDNTCLNNAIOAFNGSDVTMMQ 374

Db 356 PAPVOTTTATTTAATFRKNRP-LGPAGSENEIP-THVLPCCANLQAOGLKSNVSGSTHL 413

Qy 375 XXPXXXXTAXXXXXXRXVXXPXLXXXXXKXKXKXKXKXKXKXKXKXKXKXKXKX 434

Db 414 CLSDNDYGDGLAGASSHTTKSMAAPPSGLSLPVVFTALALLSVSLAETS 468

Qy 435 CXXXXXXKX 489

RP SEQUENCE FROM N.A.

RC STRAIN-HANOVER;

RA ZHONG J., ANNES M., HEUMANN R.;

RL SUBMITTED (OCT-1997) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: A002072; E1134274; -

SO SEQUENCE 463 AA; 51032 MW; 9327791 CRC32;

Query Match 82.6%; Score 1728; DB 11; Length 463;

Best Local Similarity 50.7%; Pred. No. 0.00e+00;

Matches 241; Conservative 12; Mismatches 208; Indels 14; Gaps 10;

Db 3 LATLYFVLPDLILMSAEVSGDRDLCVAKASDCLKEGSCSTKYRTLROCVAGKETFNLSL 62

Qy 15 LXTLSLXPLXLLXSSXXXXXXDCVAXXXCXAEXXCSXXRTLRQCGAGXXXXXX 74

Db 63 TSGLEAKDECRSAMEALOKSLYNCRCRGMKREKNCILRIYMSYSLQ-GNDLLEDSPY 121

Qy 75 XXXXXAXXEXXAXEXLXSSLYDCRCKRMKREKXCLXIYWSYXXLXGXGXXLXSPY 134

Db 122 E-PVNSRLSDIFRAVPEISV--EHIS--KGNCLDAKACNLDTCCKYRSAYITPCTT 177

Qy 135 EXPVTSRLSDIFRAXXSSXXXXXXKSNCLDAKACNLDCKRLRSATIXXXCX 194

Db 176 SMSN-EVCNRRKCHKALROFEDKVPARKSYGMFCSCR--DIACERRRQTIIVPCSYEE 237

Qy 195 XXSXXERCNRRKCHKALROFEDKVPXHXGYGMLFCSCXXMXACKERRRQTIIVPCSYEX 254

Db 238 RERNCLNLDSCKTNYICRSRLADFTNCOPEBSRVSNCLEKENYADCLLAYSGLIGTVM 297

Qy 255 XEHPNCLDLRSXCRTDYLCSRLADFTNCPXXXRXXTXCAAXNYXXCLXAYXGLIGTVM 314

Db 293 TPNTVDS-SLS-VAPMCDSCNSGNDLEDCLKFLNFNDNTCLNNAIOAFNGSDVTMMQ 350

Qy 315 TPNTVDSXXTXVAPMCDSCNSGNDLEDCLKFLNFNDNTCLNNAIOAFNGSDVTMMQ 374

Db 351 PAPVOTTTATTTAATFRKNRP-LGPAGSENEIP-THVLPCCANLQAOGLKSNVSGSTHL 408

Qy 375 XXPXXXXTAXXXXXXRXVXXPXLXXXXXKXKXKXKXKXKXKXKXKXKXKXKXKX 434

Db 409 CLSDSDYGDGLAGASSHTTKSMAAPPSGLSLPVVFTALALLSVSLAETS 463

Qy 435 CXXXXXXKX 489

RESULT 6 PRELIMINARY; PRT: 463 AA.

AC 035252; (TREMBLEREL. 05, CREATED)

DT 01-JAN-1998 (TREMBLEREL. 05, LAST SEQUENCE UPDATE)

DT 01-JAN-1998 (TREMBLEREL. 05, LAST SEQUENCE UPDATE)

DE GENE RECEPTOR BETA.

OS GDNF-BETA.

OS MUS MUSCULUS (MOUSE).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;

OC SCIUROGNATHI; MORIDAE; MORINAE; MUS.

RP SEQUENCE FROM N.A.

RC STRAIN-C57;

RA DEY B.K., MONG Y.W., TOO H.P.;

RL NEUROREPORT 9:0-0(0001).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-C57;

RA DEY B.K., MONG Y.W., TOO H.P.;

RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: AF015172; G2624963; -

SO SEQUENCE 463 AA; 51134 MW; 910E17F CRC32;

Query Match 81.8%; Score 1711; DB 11; Length 463;

Best Local Similarity 49.7%; Pred. No. 0.00e+00;

Matches 236; Conservative 19; Mismatches 206; Indels 14; Gaps 10;

Db 3 LATLYFVLPDLILMSAEVSGDRDLCVAKASDCLKEGSCSTKYRTLROCVAGKETFNLSL 62

Oy		15	LNTLTKSLTXPLLLXXXXXXXRRXXDDCVAXXCCAEYXXCSXXHTYLQCAAGXXNNX	74
Dd		63	TSGLEAKCEGCSNAMEALKQKSLINCRCRCKGMKEKNCLRTIYMSOTSIQ-GNDLEDSPY	121
Oy		75	XXXXXXXXXXECXXAEXLXXSSLYDCRCRKGMKEKXXCLXIYMSHXHXLXGXHLENSPY	134
Dd		122	E-PVNSRLSDIEFRVAVPTLSV---EHIS--KGNNCLDAACNLDDTCRKRSAYATTPTT	175
Oy		135	EXPVTSRSLDIFRXKXSXXXSXDXXXXXXSNXCIDAAACNLNDCRKLBSATITXXCXX	194
Dd		176	SMSN-EVCNRKRCKHALROFEDFKVPAAKHSYGMLFCSCR--DVACTERRROTIVPCSYEE	232
Oy		195	XXXSXXERGNRRKKHKLROGFEDKVPAXHHXGMLFGSCXXAXXDAAECERRROTIXSCSEX	254
Dd		223	RERPNCNLDDSCFTWICSSLADFEFNCOPEPSRSVSNCLKENYADCLLAYSGLIETVM	292
Oy		255	XEXPNCIDLRSXCRTDLCSRSLADFYTNCPXXRXXTJCXANXXXCIMAYXGLIGTM	314
Dd		293	TPNYTDS-SLS-VAPMCDOSNGNDLOCILFLNEFKNTCLKAIAFGSGDYTMQ	350
Oy		315	TPNYVDSXXTXYYXPAFPCXGRGSNGXEXDEKFLXXFXFNPCLNAINAFNGXDVMSQ	374
Dd		351	PAPYQTATTATTTFATFIKKP-LGPAGSENEIP-THVLPCANLOAKLSNYSGS7HL	408
Oy		375	XXPXXXTXAXXXXXXXVXXXPYLXXXXSXKXXXTYVAXXXQXXLXXNXSXXXX	434
Dd		409	CLSDNDYGDOLAGASSHITTKSMAPPCSGLSLPVWFITALALLSVSLAETS	463
Oy		435	CXXXXXXXSXXXXXXXXXXXXXSXXLXLPLVLTGLXXXXLXXLXETS	489
RESULT		7		
ID	043912	PRELIMINARY:	PRT:	465 AA.
DI	043912;			
DT	01-JUN-1998 (TREMBL.REL. 06, CREATED)			
DR	01-JUN-1998 (TREMBL.REL. 06, LAST SEQUENCE UPDATE)			
DT	01-AUG-1998 (TREMBL.REL. 07, LAST ANNOTATION UPDATE)			
DE	GPI-LINKED ANCHOR PROTEIN.			
GN	GPRAL.			
OS	HOMO SAPIENS (HUMAN).			
OC	EUFARJOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES			
CC	CATARRHINI; HOMINIDAE; HOMO.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	ANDRIST M., JING S., BULK S., BENTLEY K., NATLASAMY S., HALUSKA M.,			
TA	FOX G.M., CHAKRAVARTI A.;			
RL	GENOMICS 0:0-0(1998).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-MEDULLARY THYROID CARCINOMA TUMOR;			
RA	SHEFFELINE S.E., KHORANA S., SCHULTZ P.N., HUANG E., THOBE N., HU Z.J.,			
FO	FOX G.M., JING S., CORE G.J., GAGEL R.F.;			
HU	GENET. 0:0-0(1998).			
DR	EMBL; AF038420; G2921545.-			
DR	EMBL; AF038411; G2921545. JOINED.			
DR	EMBL; AF038412; G2921545. JOINED.			
DR	EMBL; AF038413; G2921545. JOINED.			
DR	EMBL; AF038414; G2921545. JOINED.			
DR	EMBL; AF038415; G2921545. JOINED.			
DR	EMBL; AF038416; G2921545. JOINED.			
DR	EMBL; AF038417; G2921545. JOINED.			
DR	EMBL; AF038418; G2921545. JOINED.			
DR	EMBL; AF038419; G2921545. JOINED.			
DR	EMBL; AF042080; G2801557.-			
DR	EMBL; AF038421; G2921532.-			
DR	EMBL; AF058959; G306783.-			
DR	EMBL; AF058950; G306783. JOINED.			
DR	EMBL; AF058951; G306783. JOINED.			
DR	EMBL; AF058952; G306783. JOINED.			
DR	EMBL; AF058953; G306783. JOINED.			
DR	EMBL; AF058954; G306783. JOINED.			
DR	EMBL; AF058955; G306783. JOINED.			

	Query Match	81.0%	Score 1695;	DB 4;	Length 465;
	Best Local Similarity	49.5%	Pred. No. 0.00e+00;		
	Matches 235;	Conservative 17;	Mismatches 211;	Indels 12;	Gaps 10
DR	EMBL: AF058996;	G3068783;	JOINED.		
DR	EMBL: AF058997;	G3068783;	JOINED.		
DR	EMBL: AF058998;	G3068783;	JOINED.		
SQ	SEQUENCE 465 AA;	5145 MW;	1C4EAE03 CRC32;		
Db	3	IATLYPALPLDLLLSAEVSGGDRDVCYKASDQCLEQSGCSTKYRTLROCVAGETNFSL	62		
Qy	15	LATLTLXAXPLTLXSSXXXXXXDXCVAXXXCAEXXCSXXRTLRLQCAAGAXNXX	74		
Db	63	ASGLAKDECBRSAMALQKSLYINCRCRGRKKKEKNCRLRIYWSYQSLQ-GNDLLEDSPY	121		
Qy	75	XXXXXXAXECXXAXEXLXXSSLYDCRCRGRKKKEXXCLXIYWSHXXLXXGXXLXESPY	134		
Db	122	E-PVNSRLSDIFRYVPFLSDVFOQVEHLPKNNCLDAAKCNLDICKKRYSAITTCCTT	146		
Qy	135	EYPVTSRLSDIFRYXXSXXXXXXDXNXXNCLDAAKCNLDCKKRSAYIXXCSX	151		
Db	181	SVSN-DVGNRRRCCHALROFDFDKPAKHSYMLFCSCR-DIACERRORIYVGSYE	247		
Qy	195	XXSXXERNCRRKCHALQOFFDKPXXHXIYMLFCSCAXDXAXERRORIYXSCSYEX	254		
Db	238	REKPNCLNLODSCKNTYICRSRLADFTNCOPEBSRVSCLKENYADCLLAYSLGIVH	297		
Qy	255	XEXPNCCLDRSACRDYLCRSRLADFTNCRKPPXRXXTXCXAKNXXCLAYXCLITGM	314		
Db	298	TPNTIDSS-SLS-VAPMCDCSNGDLLEBCLFLNFKNDNTCLKNAIQAFGSGSVTWQ	355		
Qy	315	TPNYDSXXTXXYAVPMCCXGSGNSXDECEKFLXFXFXNPCLXNAIQAFGNGDXVMSQ	374		
Db	356	PAFPQTATTATTLARKNKP-LGPAGSEHLP-THVLPCCANLQKLSNVSGTHL	413		
Qy	375	XXPXXXTXXAXXXXXXXRYXXAPLXXXXXXXXIXXXXXXXQXQXKLXNXXXXXX	434		
Db	414	CISNGNEKEGELGASSHTTK-SMAAPPGCLSPDLLLVYVTAALSTLS--LTENS	465		
Qy	435	CAXXXXXXXXXXXXXXXXXXXXXXAXSXXLXLLPVLMLTFLXLLXLLXLLXETS	489		

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RESULT      8
ID          015507      PRELIMINARY:
AC          015507;
DT          01-JAN-1998 (TREMBLREL, 05, CREATED)
DT          01-JAN-1998 (TREMBLREL, 05, LAST SEQUENCE UPDATE)
DT          01-NOV-1998 (TREMBLREL, 08, LAST ANNOTATION UPDATE)
DE          RET LIGAND 1.
GN          RET1.
OS          HOMO SAPIENS (HUMAN).
OC          EDUAROTA; MELIZON; CHODATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES.
CC          CATARRHINI; HOMINIDAE; HOMO.
RN          [1]
RP          SEQUENCE FROM N.A.
RC          TISSUE-KIDNEY;
RX          MEDLINE: 9732356
RA          SANICOLA M., HESSION C.A., WORLEY D.S., CARMILLO P., EHRENFELDS C.,
RA          WMLUS L., ROBINSON S., JAWORSKI G., WEI H., TIZARD R., WHITTY A.,
RA          PEPINSKY R.B., CAPE R.L.;
RT          "Glial cell line-derived neurotrophic factor-dependent RET activation
RT          can be mediated by two different cell-surface accessory proteins.";
RL          PROC. NATL. ACAD. SCI. U.S.A. 94:6238-6243(1997).
RN          [2]
RP          SEQUENCE FROM N.A.
RC          TISSUE-KIDNEY;
RA          SANICOLA M., HESSION C.A., WORLEY D.S., CARMILLO P., EHRENFELDS C.,
RA          WMLUS L., ROBINSON S., JAWORSKI G., WEI H., TIZARD R., WHITTY A.,
RA          PEPINSKY R.B., CAPE R.L.;
RL          SUBMITTED (APR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN          [3]
RP          SEQUENCE FROM N.A.
RC          TISSUE-SUBSTANTIA NIGRA;

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